

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
SEQUENCE LISTING

<110> Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.

<120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same

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<140> 09/665,350
<141> 2000-09-18

<150> PCT/US00/04414
<151> 2000-02-22

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<151> 1999-07-07

<150> US 60/145,698
<151> 1999-07-26

<150> US 60/146,222
<151> 1999-07-28

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<151> 1999-09-08

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<151> 1999-10-05

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<213> Homo sapiens

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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<211> 353
<212> PRT
<213> Homo sapiens

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20 25 30
Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
35 40 45
Ala Lys Lys Asn Phe Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
50 55 60
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
65 70 75 80
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
85 90 95
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
100 105 110
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
115 120 125
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
130 135 140
Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160
Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175
Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190
His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205
Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220
Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240
Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255
Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270
Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285
Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 290 295 300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
 305 310 315 320

Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
 325 330 335

Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
 340 345 350

Leu

<210> 3
 <211> 2206
 <212> DNA
 <213> Homo sapiens

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<210> 4
 <211> 379
 <212> PRT
 <213> Homo sapiens

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 Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro Pro Gln
 20 25 30
 Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
 35 40 45
 Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
 50 55 60
 Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
 65 70 75 80
 Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
 85 90 95
 Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
 100 105 110
 Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
 115 120 125
 His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
 130 135 140
 Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
 145 150 155 160
 Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
 165 170 175
 Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
 180 185 190
 Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
 195 200 205
 Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
 210 215 220
 Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
 225 230 235 240
 Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
 245 250 255
 Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
 260 265 270
 Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
 275 280 285
 Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
 290 295 300
 Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
 305 310 315 320
 His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
 325 330 335

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Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
340 345 350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 6

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21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 7

taagtccggc acattacagg tc

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<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 8

cccacatgt atgaatggtg gactttgtgt gactcctgggt ttctgcac

49

<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 9
aaagacgcat ctgcgagtgt cc 22

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Synthetic oligonucleotide probe

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<210> 11
<211> 2197
<212> DNA
<213> Homo sapiens

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<210> 12
<211> 164
<212> PRT
<213> Homo sapiens

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His Leu Ala Leu Gly Ala Gln Gln Gly Arg Gly Arg Arg Glu Leu Ala
20 25 30
Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
35 40 45
Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
50 55 60
Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
65 70 75 80
Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
85 90 95
Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
100 105 110
Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
115 120 125
Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
130 135 140
Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
145 150 155 160
His Asp Pro Gly

<210> 13
<211> 533
<212> DNA
<213> Homo sapiens

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<222> (33)..(33)
<223> a, t, c or g

<220>
<221> modified_base
<222> (37)..(37)
<223> a, t, c or g

<220>
<221> modified_base
<222> (80)..(80)
<223> a, t, c or g

<220>
<221> modified_base
<222> (94)..(94)
<223> a, t, c or g

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<222> (144)..(144)
<223> a, t, c or g

<220>
<221> modified_base
<222> (188)..(188)
<223> a, t, c or g

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ccaccacgag caggcgtgcc gcgntggcg ttcgtatggt gcctgggtgt tcctgcgtcg 180
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tgcccactgc cccaaacagt atgttaataa caatgacatc taccaggta ctcctgtcta 360
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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 14
ttcgaggcct ctgagaagtg gccc 24

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 15
ggcgatatct ctctggcctc cc 22

<210> 16
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 16
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<210> 17
<211> 960
<212> DNA
<213> Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ggggggagcag	tgcggaccc	cgcgcatcc	cgcagttggc	ctcctgacc	tcatcagcaa	180
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cacgtgtgt	gacaccgact	tgtgcaacgc	cagcggggcc	catgccc	agccggctgc	300
cgccatccct	gcgctgctcc	ctgcactcg	cctgctgctc	tggggaccc	gccagctata	360
ggctctgggg	ggcccccgtg	cagcccacac	tgggtgtgg	gccccaggcc	tctgtgccac	420
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gtctgaccat	gtatgtctgc	accctgtcc	cccacccctga	ccctccatg	gccccctcca	540
ggactcccac	ccggcagatc	agctctagtg	acacagatcc	gcctgcagat	gccccctcca	600
accctctctg	ctgtgtttc	catggcccg	cattctccac	ccttaaccct	gtgtctaggc	660
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ccgtgggtgc	ccccgcaccc	agcaggggac	aggcactcg	gagggcccag	taaaggctga	780
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agagatgggg	cctggaggcc	tggaggaagg	ggccaggcc	cacattcg	gggctccctg	900
aatggcagcc	ttagcacagc	gtagggccctt	aataaacacc	tgttgataa	gccccaaaaa	960

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
1 5 10 15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
20 25 30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
35 40 45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
50 55 60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
65 70 75 80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
85 90 95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
100 105 110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
115 120 125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
130 135 140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
145 150 155 160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
165 170 175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
180 185

<210> 19

<211> 24

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 19

tgcttgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

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gaccgaccag	ctgagcag	ggcagatccg	cgagttacaa	ctctacagca	ggaccagtgg	180
caagcacgt	cagg	tcgtc	ggcaggtgg	gcaacaagt	240	
tgccaagtc	atagtggaga	cgacacgtt	tggcagccgg	gttcgcata	aaggggctga	300
gagtgagaag	tacatctgt	tgaacaagag	gggcaagtc	atcgggaa	ccagcgggaa	360
gagcaaagac	tgcgtttca	cgagatcgt	gctggagaac	aactatacgg	cttccagaa	420
cggccggcac	gagg	tcatggc	cacgcggcag	gggcggcccc	gccaggcttc	480
ccgcagccgc	cagaacc	gcgaggcc	cttcatcaag	cgcctctacc	aaggccagct	540
gcccttcccc	aaccacg	agaagcagaa	gcagttcgag	tttggggct	ccgccccac	600
ccgcccggacc	aagcgcac	ggcggcccc	gcccctca	tagtctggg	ggcagggggc	660
agcagcccc	ggccgc	cccaccc	tcccttctt	atccaaggac	tgggctggg	720
tggcgggagg	ggagcc	ccccgagg	ggaccctgag	ggccgcga	atcccgagcc	780
cccagctgg	aa	ggggcagg	ccgg	ggggcgct	cccttcc	840
gacgggtggc	agg	ccctgt	gaggaactga	gtgtcac	caccagc	900
tgccggcctc	ccagccgg	tcctg	cgctgaaagg	tcagcgact	aaggccttgc	960
agacaaccgt	ctggagg	ctgt	aatctgc	tcggatct	ctcagtct	1020
ccccagcccc	caa	actc	ctggctagac	tgttagga	ttttgtt	1080
tttcaggaaa	aa	agag	agagagag	aaatagaggg	ttgtccact	1140
acgacc	cctgcac	cccc	act	cccagcccc	ctcacattc	1200

<210> 23

<211> 205

<212> PRT

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo sapiens

<400> 23

Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
1 5 10 15

Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
20 25 30

Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
50 55 60

Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
100 105 110

Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
115 120 125

Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
130 135 140

Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
165 170 175

His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
180 185 190

Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
195 200 205

<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 25
ccggtagacct gcacgtgctt gccaa

24

<210> 26
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>
<221> modified_base
<222> (21)..(21)
<223> a, t, c or g

<400> 26
gcggatctgc cgcctgctca nctggtcggt catggcgccc t

41

<210> 27
<211> 2479
<212> DNA
<213> Homo sapiens

<400> 27
acttgcctatc acctgttgcg agtgtggaaa aattctccct gttgaatttt ttgcacatgg 60
aggacagcag caaagagggc aacacaggct gataagacca gagacagcag ggagattatt 120
ttaccatacg ccctcaggac gttccctcta gctggaggtc tggacttcaa cagaacccca 180
tccagtcatt ttgatttgc tgtttatttt ttttttctt ttctttttcc caccacattg 240
tattttattt ccgtacttca gaaatgggcc tacagaccac aaagtggccc agccatgggg 300
ctttttcctt gaagtcttgg cttatcattt ccctggggct ctactcacag gtgtccaaac 360
tcctggcctg cccttagtgtg tgccgctgctg acaggaactt tgcactactgt aatgagcgaa 420
gcttgacctc agtgccttcc gggatcccgg agggcgtaac cgtactctac ctccacaaca 480
accaaattaa taatgctgga tttccctgcag aactgcacaa tgcactgtcg gtgcacacgg 540
tctacctgta tggcaaccaa ctggacgaat tccccatgaa ccttcccaag aatgtcagag 600
ttctccattt gcaggaaaac aatattcaga ccatttcacg ggctgctctt gcccagctct 660
tgaagcttga agagctgcac ctggatgaca actccatatac cacagtgggg gtggaagacg 720
gggccttccg ggaggctatt agcctcaaatt tgggtttttt gtctaagaat caccctgagca 780
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ggaaccttcc gaccaacaag ggtatgcggc agggcacctt cagccatctc accaagctca 960
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gaagctacac gcctccaact cttaccacat cggaaacttcc cacgattctt gactggatg 1500
gcagagaaag agtgcacccca ctttttctg aacggatcca gctctctatc cattttgtga 1560
atgataacttc cattcaagtgc agctggctct cttctttcac cgtgatggca tacaactca 1620
catgggtgaa aatgggcccac agtttagtag ggggcatctgt tcaggagcgc atagtcagcg 1680
gtgagaagca acacctgagc ctggtaact tagagccccgg atccacctat cggattttgtt 1740
tagtgcctact ggatgtttt aactaccgcg cggtagaaga caccattttgt tcagaggcca 1800
ccaccatgc ctcctatctg aacaacggca gcaacacacgc gtccagccat gaggcagacg 1860
cgtcccacag catgggctcc ccctttctgc tggcgggctt gatggggggc gcggtgatat 1920
tttgtctgtt ggtcttgc tgcgtttt gctggcatat gcacaaaaag gggcgctaca 1980
cctcccaagaa gtggaaatc aaccggggcc ggcggaaatc tgattttgc gaggcaggca 2040
ccaagaagga caactccatc ctggagatga cagaaaccag ttttcatgc gtctccctaa 2100
ataacgatca actccttaaa ggagatttca gactgcagcc catttacacc ccaaattgggg 2160
gcatttaatta cacagactgc catatccccca acaacatgcg atactgcaac agcagcgtgc 2220

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cagacctgga gcactgccc acgtgacagc cagaggccca gcgttatcaa ggcggacaat 2280
 tagactctt agaacacact cgtgttgca cataaagaca cgcagattac atttgataaa 2340
 tgttacacag atgcatttgt gcattgaat actctgtaat ttatacggtg tactatataa 2400
 tgggatttaa aaaaagtgt atctttctt tttcaagttt attacaaaca gttttgttaac 2460
 tcttgctt ttaaatctt 2479

<210> 28

<211> 660

<212> PRT

<213> Homo sapiens

<400> 28

Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
 1 5 10 15

Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
 20 25 30

Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45

Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
 50 55 60

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65 70 75 80

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
 85 90 95

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
 100 105 110

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140

Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160

Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175

Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190

Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205

Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220

Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240

Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255

Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
 275 280 285
 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
 290 295 300
 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
 305 310 315 320
 Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
 325 330 335
 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
 340 345 350
 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro
 355 360 365
 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
 370 375 380
 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
 385 390 395 400
 Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg
 405 410 415
 Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
 420 425 430
 Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
 435 440 445
 Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
 450 455 460
 Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
 465 470 475 480
 Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
 485 490 495
 Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
 500 505 510
 Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
 515 520 525
 His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
 530 535 540
 Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
 545 550 555 560
 Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
 565 570 575
 Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
 580 585 590
 Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
 595 600 605

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
610 615 620

Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
625 630 635 640

Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
645 650 655

His Cys His Thr
660

<210> 29

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29

cgttctacct gtatggcaac c

21

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30

gcaggacaac cagataaacc ac

22

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31

acgcagattt gagaaggctg tc

22

<210> 32

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32

ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac

46

<210> 33

<211> 3449

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo sapiens

<400> 33

actggagca agccggcgcc gcgagacag aggcagaggc agaaagctggg gctccgtcct 60
cgccccac gagcgtccc cgaggagac cgccggccct ggcgaggcga agaggccgac 120
gaggaagacc cgggtggctg cgccccgtc tcgcttcca ggcgccggcg gctcagcc 180
tgccccctt gctgccttg aaaatggaaa agatgctcgc aggctgctt ctgctgatcc 240
tcggacagat cgtcctctc cctgcccagg ccaggagcg gtcacgtggg aggtccatct 300
ctagggcag aacacgtcgg acccaccgcg agacggccct tctggagagt tcctgtgaga 360
acaaggccc agacctggtt ttcatcattg acagctctcg cagtgtaac acccatgact 420
atgcaaaggt caaggagttc atcgtggaca tcttgcattt ctggacatt ggtcctgtatg 480
tcacccgagt gggctgctc caaatggca gcaactgtcaa gaatgagttc tcccctaaga 540
ccttcaagag gaagtcccgag gtggagcgtg ctgtcaagag gatgcggcat ctgtccacgg 600
gcaccatgac tggctggcc atccagtatg ccctgaacat cgcattctca gaagcagagg 660
gggcccggcc cctgaggagg aatgtccac gggtaataat gatcgtgaca gatgggagac 720
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tcatcaacga gggactcaag acctgtccc ggggtggatta ctgc当地 1560
gttgtgaata ctccctgtgtc aacatggaca gatccttgc ctgtc当地 1620
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gtatatggat gtatgc当地 aatcatagga catatgtact ttttttgc当地 gttggattttt 3420
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<210> 34

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 915
<212> PRT
<213> Homo sapiens

<400> 34
Met Glu Lys Met Leu Ala Gly Cys Phe Leu Leu Ile Leu Gly Gln Ile
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Val Leu Leu Pro Ala Glu Ala Arg Glu Arg Ser Arg Gly Arg Ser Ile
20 25 30
Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
35 40 45
Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
50 55 60
Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65 70 75 80
Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95
Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
100 105 110
Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
115 120 125
His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
130 135 140
Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145 150 155 160
Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
165 170 175
Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
180 185 190
Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205
Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
210 215 220
Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
225 230 235 240
Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
245 250 255
Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
260 265 270
Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
275 280 285
Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
290 295 300
Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305 Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
 310 325 330 335
 Val 325
 Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
 340 345 350
 Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn
 355 360 365
 Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
 370 375 380
 Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
 385 390 395 400
 Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
 405 410 415
 Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
 420 425 430
 Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
 435 440 445
 Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
 450 455 460
 Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
 465 470 475 480
 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
 485 490 495
 His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
 500 505 510
 Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
 Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp
 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys
 580 585 590
 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile
 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
645 650 655

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn
660 665 670
Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly
675 680 685
Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
690 695 700
Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
705 710 715 720
Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
725 730 735
Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
740 745 750
Val Gly Lys Ala Ile Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
755 760 765
Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
770 775 780
Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
785 790 795 800
Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
805 810 815
Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
820 825 830
Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
835 840 845
Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
850 855 860
Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
865 870 875 880
Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
885 890 895
Arg Leu Glu Glu Met Thr Gln Arg Met Glu Ala Leu Glu Asn Arg Leu
900 905 910
Arg Tyr Arg
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 35

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

45

<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

ggagccgccc	tgggtgtcag	cggctcggt	cccgcgacg	ctccggccgt	cgcgcagcct	60
cgccacccgtc	agggtccgtc	gtccccggc	tggcgccccc	gactccgtcc	cggccaggga	120
gggcacatgt	ttccctcccg	gggcggctgg	tgaccaactt	gctgcgggtt	ttgttccctgg	180
ggctgagtgc	cctcgcgccc	ccctcgcggg	cccagctgca	actgcacttg	cccgcccaacc	240
ggttgcaggc	ggtggaggga	ggggaaatgg	tgcttccagc	gtggtacacc	ttgcacgggg	300
agggtgtctc	atcccagcca	tgggaggtgc	cctttgtat	gtggttcttc	aaacagaaaag	360
aaaaggagga	tcaagggttg	tcctacatca	atggggtcac	aacaagcaaa	cctggagat	420
ccttggtcta	ctccatgccc	tcccggaaacc	tgtccctgct	gctggagggt	ctccaggaga	480
aagactctgg	ccccctacagc	tgctccgtga	atgtgcaaga	caaacaaggc	aatcttaggg	540
gccacacgt	caaaacctt	gaactcaatg	tactggttcc	tccagctcct	ccatcctgcc	600
gtctccaggg	tgtccccat	gtggggggaa	acgtgaccc	gagctgccc	tctccaagga	660
gtaagccgc	tgtccaatac	cagtgggatc	ggcagcttcc	atcccttccag	actttctttg	720
caccaggatt	agatgtcatc	cgtgggtctt	taagcctc	caacctttcg	tcttccatgg	780
ctggagtc	tgtctgcaag	gcccacaatg	aggtgggcac	tgcccaatgt	aatgtgacgc	840
tggaaagttag	cacagggcct	ggagctgcag	tgggtgtctt	agctgttgt	ggtaccctgg	900
ttggactggg	gttgcgtgt	gggctgggtc	tcttgcacca	ccggccggggc	aaggccctgg	960
aggagccagc	caatgatatac	aaggaggatg	ccattgc	ccggacccctg	ccctggccca	1020
agagctcaga	cacaatctcc	aagaatggg	ccctttcc	tgtcacctcc	gcacgagccc	1080
tccggccacc	ccatggccct	cccaggcctg	gtgcattgac	ccccacgccc	agtctctcca	1140
gccagccct	gccctcacca	agactgccc	cgacagatgg	ggcccaccc	caaccaat	1200
ccccatccc	tggtggggtt	tcttcctct	gcttgagcc	catgggtgt	gtgcctgt	1260
tggtgctgc	ccagagtcaa	gctggctct	tggtatgt	accccaccac	tcattggct	1320
aaggattttgg	ggtctctct	tcctataagg	gtcacctct	gcacagaggc	ctgagtcat	1380
ggaaagagtc	acactcctga	cccttagtac	tctgccccca	cctcttta	ctgtgggaaa	1440
accatctcg	taagacctaa	gtgtccagga	gacagaagga	gaagaggaag	tggatctgga	1500
attgggagga	gcctccaccc	accctgtact	cctccctttag	aaggcagctg	ctgaaattag	1560
ctactcacca	agagtgggg	gcagagactt	ccagtca	agtctccag	gcccccttga	1620
tctgtatccc	acccttatct	aacaccaccc	ttggctccca	ctccagctcc	ctgtatttgc	1680
ataacctgtc	aggctggctt	ggttaggttt	tactggggca	gaggataggg	aatctcttat	1740
taaaactaac	atgaaatatg	tgttggtttc	atttgcaaaat	ttaaataaaag	atacataata	1800
tttgtatgaa	aaa					1813

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 39
<211> 390
<212> PRT
<213> Homo sapiens

<400> 39
Met Ile Ser Leu Pro Gly Pro Leu Val Thr Asn Leu Leu Arg Phe Leu
1 5 10 15
Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser Arg Ala Gln Leu Gln
20 25 30
Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Glu Val
35 40 45
Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
50 55 60
Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
65 70 75 80
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
85 90 95
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
100 105 110
Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
115 120 125
Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
130 135 140
Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
145 150 155 160
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
165 170 175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
180 185 190
Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
195 200 205
Leu Ser Leu Thr Asn Leu Ser Ser Met Ala Gly Val Tyr Val Cys
210 215 220
Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
225 230 235 240
Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
245 250 255
Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
260 265 270
Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
275 280 285
Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
290 295 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40
agggtctcca ggagaaagac tc 22

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41
attgtgggcc ttgcagacat agac 24

<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 42
ggccacagca tcaaaacctt agaactcaat gtactggttc ctccagctcc 50

<210> 43
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 43
gtgtacaca gcgtggc 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 44
gaccggcagg cttctgct 18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 45
cagcagcttc agccaccagg agtgg 25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 46
ctgagccgtg ggctgcagt tcgc 24

<210> 47
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 47
ccgactacga ctggttcttc atcatgcagg atgacacata tgtgc 45

<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
cgccaccact gcccacccg ccaatgaaac gcctcccgct cctagtggtt tttccactt 60
tggtaattt ttcctataact caaaatttgc ccaagacacc ttgtctccca aatgcaaaat 120
gtgaaatacg caatggatt gaaggctgct attgcaacat gggattttca ggaaatggtg 180
tcacaatttg tgaagatgtt aatgaatgtt gaaatttaac tcagtcctgt ggcggaaaatg 240
ctaattgcac taacacagaa ggaagttattt attgtatgtt tgtacctggc ttcagatcca 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gcagtaacca agacagggtt atcactaatg atggaaccgt ctgtatagaa aatgtgaatg 360
 ccaaactgcca tttagataat gtctgtatag ctgcaaataat taataaaaact ttaacaaaaa 420
 tcagatccat aaaagaacct gtggcttgc tacaagaagt ctatagaaat tctgtacag 480
 atctttcacc aacagatata attacatata tagaaatatt agctgaatca tcttcattac 540
 taggttacaa gaacaacact atctcagcca aggacacccct ttcttaactca actcttactg 600
 aatttgtaaa aaccgtgaat aattttgttc aaagggatac attttagtgg tgggacaagt 660
 tatctgtgaa tcataggaga acacatctta caaaactctt gcacactgtt gaacaagcta 720
 cttaaggat atccccagagc ttccaaaaga ccacagagtt tgataacaat tcaacggata 780
 tagctctcaa agtttctt tttgttcat ataacatgaa acatattcat cctcatatga 840
 atatggatgg agactacata aatatatttc caaagagaaaa agctgcataat gattcaaatg 900
 gcaatgtgc agttgcattt ttatattata agagtattgg tccttgctt tcatcatctg 960
 acaacttctt attgaaacact caaaattatg ataattctga agaggaggaa agagtcatat 1020
 cttcagtaat ttcaagtctca atgagctaa acccaccac attatatgaa cttgaaaaaaa 1080
 taacatttac attaagtcat cgaaaggta cagataggta taggagtcta tgcattttt 1140
 ggaattactc acctgatacc atgaatggca gctggcttc agagggctgt gagctgacat 1200
 actcaaatga gaccacaccc tcatgccct gtaatcacct gacacatttt gcaattttga 1260
 tgtcctctgg tccttccatt ggtattaaag attataatat tcttacaagg atcaactcaac 1320
 taggaataat tatttcactg atttgcattt ccataatgcatt ttttaccttc tggttcttca 1380
 gtgaattca aagcaccagg acaacaattt acaaaaatct ttgcattgtc tattttctt 1440
 ctgaacttgt ttttcttgc gggatcaata caaataactaa taagctctt ttttcaatca 1500
 ttgcccggact gctacactac ttcttttag ctgcattttgc atggatgtgc attgaaggca 1560
 tacatctcta tctcattgtt gtgggtgtca tctacaacaa gggatttttg cacaagaatt 1620
 tttatatctt tggctatcta agcccgccg tggtagtgg attttcggca gcactaggat 1680
 acagatatta tggcacaacc aaagatgtt ggcttagcac cggaaacaac tttatggaa 1740
 gtttatagg accagcatgc ctaatcattt ttgttaatct cttggctttt ggagtcatca 1800
 tatacaaagt ttttcgtcac actgcagggt tggaaaccaga agttagttgc tttgagaaca 1860
 taaggcttg tgcagagaga gcccgcgc ttctgttcc tctcggcacc acctggatct 1920
 ttggggtttccatgttgc cacgcatcg tggtagtgc ttacctctt acagtcatca 1980
 atgcttcca gggatgttc attttttat tcctgtgtt tttatctaga aagattcaag 2040
 aagaatatta cagattgttcc aaaaatgtcc cctgttgc tggatgttta aggtaaacat 2100
 agagaatggt ggataattac aactgcacaa aaataaaaaat tccaagctgt ggatgaccaa 2160
 tgtataaaaaa tgactcatca aattatccaa ttattaacta ctagacaaaaa agtattttaa 2220
 atcagttttt ctgtttatgc tataggact gtagataata aggtaaaatt atgtatcata 2280
 tagataatact atgtttttct atgtgaaata gttctgtcaa aaatagtatt gcagatattt 2340
 gggaaatgtt tggtttctca ggagtgatat cactgcaccc aaggaaagat ttttttctt 2400
 acacgagaag tataatgtt tcctgttgc aaccactggc ttgtatattt tgcactcgt 2460
 gttgccttc aactagtcc cctaccaccc cggtaatgag ctccattaca gaaagtggaa 2520
 cataagagaa tgaaggggca gaatatcaaa cagtggaaag ggaatgataa gatgtatattt 2580
 gaatgaactg tttttctgt agactagctg agaaattgtt gacataaaaat aaagaattga 2640
 agaaacacat ttaccatt tgcattgt tctgaactt aatgtccact aaaacaactt 2700
 agactctgt ttgcataatc tggctttt tctaataattt taaaaaaaaaaa aaaaagggtt 2760
 acctccacaa attgaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa aaaaaaaaaaaa 2820
 aa 2822

<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

Met	Lys	Arg	Leu	Pro	Leu	Leu	Val	Val	Phe	Ser	Thr	Leu	Leu	Asn	Cys
1				5				10				15			

Ser	Tyr	Thr	Gln	Asn	Cys	Thr	Lys	Thr	Pro	Cys	Leu	Pro	Asn	Ala	Lys
							20		25			30			

Cys	Glu	Ile	Arg	Asn	Gly	Ile	Glu	Ala	Cys	Tyr	Cys	Asn	Met	Gly	Phe
							35		40		45				

Ser	Gly	Asn	Gly	Val	Thr	Ile	Cys	Glu	Asp	Asp	Asn	Glu	Cys	Gly	Asn
							50		55		60				

Leu	Thr	Gln	Ser	Cys	Gly	Glu	Asn	Ala	Asn	Cys	Thr	Asn	Thr	Glu	Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

65 70 75 80

Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
85 90 95Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
100 105 110Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
115 120 125Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
130 135 140Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
145 150 155 160Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Ser Leu Leu Gly Tyr Lys
165 170 175Asn Asn Thr Ile Ser Ala Lys Asp Thr Leu Ser Asn Ser Thr Leu Thr
180 185 190Glu Phe Val Lys Thr Val Asn Asn Phe Val Gln Arg Asp Thr Phe Val
195 200 205Val Trp Asp Lys Leu Ser Val Asn His Arg Arg Thr His Leu Thr Lys
210 215 220Leu Met His Thr Val Glu Gln Ala Thr Leu Arg Ile Ser Gln Ser Phe
225 230 235 240Gln Lys Thr Thr Glu Phe Asp Thr Asn Ser Thr Asp Ile Ala Leu Lys
245 250 255Val Phe Phe Phe Asp Ser Tyr Asn Met Lys His Ile His Pro His Met
260 265 270Asn Met Asp Gly Asp Tyr Ile Asn Ile Phe Pro Lys Arg Lys Ala Ala
275 280 285Tyr Asp Ser Asn Gly Asn Val Ala Val Ala Phe Leu Tyr Tyr Lys Ser
290 295 300Ile Gly Pro Leu Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln
305 310 315 320Asn Tyr Asp Asn Ser Glu Glu Glu Arg Val Ile Ser Ser Val Ile
325 330 335Ser Val Ser Met Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys
340 345 350Ile Thr Phe Thr Leu Ser His Arg Lys Val Thr Asp Arg Tyr Arg Ser
355 360 365Leu Cys Ala Phe Trp Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp
370 375 380Ser Ser Glu Gly Cys Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser
385 390 395 400

Cys Arg Cys Asn His Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
405 410 415

Pro Ser Ile Gly Ile Lys Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln
420 425 430
Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr
435 440 445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys
450 455 460
Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465 470 475 480
Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
485 490 495
Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510
Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525
Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540
Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560
Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575
Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590
Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620
Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640
Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655
Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670
Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685
Leu Arg
690

<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<222> (61)..(61)
<223> a, t, c or g

<400> 50
tggaaacata tcctccctca tatgaatatg gatggagact acataaataat atttccaaag 60
ngaaaagccg gcatatggat tcaaatggca atgttgcagt tgcatttttta tattataaga 120
gtatttgtcc ctttgcttgc atcatctgac aacttcttgc taaaacctca aaattatgtat 180
aattctgaag aggaggaag agtcatatct tcagtaatttt cagtcataat gagctcaaac 240
ccacccacat tatatgact tgaaaaata acatttacat taagtcatcg aaaggtcaca 300
gataaggata ggagtctatg tggcatttg gaatactcac ctgataccat gaatggcagc 360
tggtcttcag agggctgtga gctgacatac tcaaatgaga cccacacctc atgccgctgt 420
aatcacctga cacatttgc aattttgat tcctctgtc cttccattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgtat ttgtcttgcc 540
atatgcattt ttaccttctg gttcttcagt gaaattcaaa gcaccagga 589

<210> 51
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 51
ggtaatgagc tccattacag 20

<210> 52
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 52
ggagtagaaa gcgcatgg 18

<210> 53
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 53
cacctgatac catgaatggc ag 22

<210> 54
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 54
cgagctcgaa ttaattcg 18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 55
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 55
 ggatccctg agtcagg

18

<210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 56
 cctagttgag tgatccttgt aag

23

<210> 57
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 57
 atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt

50

<210> 58
 <211> 2137
 <212> DNA
 <213> Homo sapiens

<400> 58
 gctcccgcc aagaacctcg gggccgctgc gcgggtgggaa ggagttcccc gaaacccggc 60
 cgctaagcga ggcctcctcc tcccgcagat cgcAACgcgc tggcggggtt caccggcgtt 120
 gggacaagaa gccgcgcctt gcctgcccgg gcccggggag gggctgggg ctggggccgg 180
 aggcgggggtg tgagtgggtg tgtgcggggg gcggagggtt gatgcataatcc cgataagaaa 240
 tgctcggtg tcttgggacac ctacccgtgg gggccgttaag gcgtactat ataaggctgc 300
 cggccggag cgcgcgcgc gtcagagcag gagcgtctcg tccaggatct agggccacga 360
 ccatccaaac cccgcactca cagccccgca ggcgcattcc gtcgcgcgc agcctccgc 420
 acccccattcg cccggactgc gccgagagcc ccagggaggt gccatgcggaa gcgggtgtgt 480
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 cttctcgac gccccccccc acgtgcacta cggctgggc gaccccatcc gcctgcggca 600
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 cgtcggtgac tgcgcgcggg gccagagcgc gcacagttt ctggagatca aggcagtcgc 720
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tggcgccga 780
 cggcaagatg caggggctgc ttcaagtactc ggaggaagac tggctttcg aggaggagat 840
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgccctccgg tctccctgag 900
 cagtgccaa cagcggcagc tgtacaagaa cagaggcttt ctccactct ctcatttcct 960
 gcccattgtc cccatggtcc cagaggagcc tgaggaccc agggccact tggaaatctga 1020
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 agtccacgtt ctgttttagct ttaggaagaa acatctagaa ttgtacata ttcaagat 1260

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gctgca	ctc	actgt	ctcagttctg	cttgaatacc	tccatcgatg	ggaaactcac	ttcccttgg	1440
aaaattctt	a	tgtcaagctg	aaattctcta	atttttctc	atcacttccc	caggagcagc	1500	
cagaagacag	gc	ca	gtagttt	taatttcagg	aacaggtat	ccactctgt	aaacagcagg	1560
taaatttcc	cac	tca	acccat	gtgggaattt	atctatatct	ctacttccag	ggaccattt	1620
cccttccaa	at	cc	cctccag	gccagaactg	actggagcag	gcatggccca	ccaggcttca	1680
ggagttaggg	a	gg	ggatggag	ccccactcca	gcccgggac	aacttgagaa	ttccccctga	1740
ggccagg	tt	tc	catggat	ctgtcctgag	aataacttgc	tgtccgggt	tcacctgtt	1800
ccatcttcc	a	cc	caccaggc	cctctgccc	cctcacatgc	ctccccatgg	attggggcct	1860
cccaggcccc	c	cc	ccatctatg	tcaacctgca	cttcttgttc	aaaaatcagg	aaaagaaaaag	1920
atttgaagac	c	cc	caagtc	gtcaataact	tgctgtgtgg	aagcagcggg	ggaagaccta	1980
gaacccttc	cc	cc	cagcactt	ggtttccaa	catgatattt	atgagtaatt	tatttgata	2040
tgtacatctc	tt	at	tttctt	acattat	tttgccccc	ttatatttat	gtatgtaa	2100
gaggtttgg	tt	tg	tatatta	aatggagtt	ttttgt			2137

<210> 59

<211> 216

<212> PRT

<213> Homo sapiens

<400> 59

Met	Arg	Ser	Gly	Cys	Val	Val	Val	His	Val	Trp	Ile	Leu	Ala	Gly	Leu
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Trp	Leu	Ala	Val	Ala	Gly	Arg	Pro	Leu	Ala	Phe	Ser	Asp	Ala	Gly	Pro
			20				25					30			

His	Val	His	Tyr	Gly	Trp	Gly	Asp	Pro	Ile	Arg	Leu	Arg	His	Leu	Tyr
		35				40					45				

Thr	Ser	Gly	Pro	His	Gly	Leu	Ser	Ser	Cys	Phe	Leu	Arg	Ile	Arg	Ala
				50			55				60				

Asp	Gly	Val	Val	Asp	Cys	Ala	Arg	Gly	Gln	Ser	Ala	His	Ser	Leu	Leu
					65			70		75				80	

Glu	Ile	Lys	Ala	Val	Ala	Leu	Arg	Thr	Val	Ala	Ile	Lys	Gly	Val	His
					85				90				95		

Ser	Val	Arg	Tyr	Leu	Cys	Met	Gly	Ala	Asp	Gly	Lys	Met	Gln	Gly	Leu
				100			105					110			

Leu	Gln	Tyr	Ser	Glu	Glu	Asp	Cys	Ala	Phe	Glu	Glu	Ile	Arg	Pro
					115		120				125			

Asp	Gly	Tyr	Asn	Val	Tyr	Arg	Ser	Glu	Lys	His	Arg	Leu	Pro	Val	Ser
				130		135				140					

Leu	Ser	Ser	Ala	Lys	Gln	Arg	Gln	Leu	Tyr	Lys	Asn	Arg	Gly	Phe	Leu
				145			150			155				160	

Pro	Leu	Ser	His	Phe	Leu	Pro	Met	Leu	Pro	Met	Val	Pro	Glu	Glu	Pro
					165			170			175				

Glu	Asp	Leu	Arg	Gly	His	Leu	Glu	Ser	Asp	Met	Phe	Ser	Ser	Pro	Leu
					180		185					190			

Glu	Thr	Asp	Ser	Met	Asp	Pro	Phe	Gly	Leu	Val	Thr	Gly	Leu	Glu	Ala
				195			200				205				

Val	Arg	Ser	Pro	Ser	Phe	Glu	Lys
				210		215	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 60
atccgcccag atggctacaa tgtgtta 26

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 61
gcctcccggt ctccctgagc agtgc当地 aac agcggcagtg ta 42

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 62
ccagtc当地 gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
cccagaagtt caaggcccccc cggcctcctg cgctcctgcc gccgggaccc tcgacccct 60
cagagcagcc ggctgcccggcc ccggaaagat ggcgaggagg agccgcccacc gcctccctcct 120
gctgctgctg cgctacctgg tggctgcccct gggctatcat aaggcctatg gttttctgc 180
cccaaaagac caacaagtag tcacagcagt agatcacaa gaggttattt tagcctgcaa 240
aaccctaaag aagactgttt cctccagatt agatggaaag aaactgggtc ggagtgtctc 300
ctttgtctac tatcaacaga ctcttcaagg tgatttaaa aatcgagctg agatgataga 360
tttcaatatac cggatcaaaa atgtgacaag aagtgtatcg gggaaatatc gttgtgaagt 420
tagtccccca tcttagcaag gccaaaacctt ggaagaggat acagtcactc tggaaatgtt 480
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agagctacga tgtcaagaca aagaaggaa tccagctctt gaatacacat gtttaagga 600
tggcatccgt ttgcttagaaa atcccaagact tggctccca agcaccaaca gctcatacac 660
aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
atattctgtt gaagccccca attctgttgg atatcgccagg tggcttggga aacgaatgca 780
agtagatgtt ctcaacataa gtggcatcat agcagccgtt gtagttgtgg ccttagtgat 840
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ctccctccag aagagaattt cttcatctaa agccacgaca atgatgtaaa atgtgcagtg 960
gctcacgcctt gtaatccccag cacttggaa ggccgcggcg ggcggatcac gaggtcaggg 1020
gttcttagacc agtctggcca atatggtaa accccatctc tactaaaata caaaaattag 1080
ctggccatgg tggcatgtgc ctgcagttcc agtgc当地 tgg gagacaggag aatcacttga 1140
acccgggagg cggagggttgc agtgc当地 gatcaca gcca ctgcagttcc gcctggtaa 1200

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260
 tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64
 <211> 312
 <212> PRT
 <213> Homo sapiens

<400> 64
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 Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
 20 25 30
 Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
 35 40 45
 Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
 50 55 60
 Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
 65 70 75 80
 Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
 85 90 95
 Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
 100 105 110
 Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
 115 120 125
 Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
 130 135 140
 Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
 145 150 155 160
 Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
 165 170 175
 Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
 180 185 190
 Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
 195 200 205
 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
 210 215 220
 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
 225 230 235 240
 Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
 245 250 255
 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
 260 265 270
 Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
 290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe
 305 310

<210> 65
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 65
 atcgttgtga agtttagtgcc cc 22

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 66
 acctgcata tccaaacagaa ttg 23

<210> 67
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 67
 ggaagaggat acagtcactc tggaaagtatt agtggctcca gcagttcc 48

<210> 68
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 68
 gacatcgagg gtgggcttagc actgaaaactg cttttcaaga cgaggaagag gaggagaaaag 60
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 gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
 aaataaaatga attactcaat ctcctatgac catctataca tactccaccc tcaaaaagta 240
 catcaatatt atatcattaa ggaaatagta accttctt ctccaaatatg catgacattt 300
 ttggacaatg caatttgtggc actggcactt atttcagtgaa agaaaaactt tgggttctta 360
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 tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtagc 540
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 taactttccc agccagattt ccagctaaaca cacagattt tctcctacag actaacaata 720
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 aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcccttctg 840
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acttacaaga actctatatt aatcacaact tgcttctac aatttcacct ggagccttta 960
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 gtaagtgggt tgatgctctt ccaaatctag agattctgtat gattggggaa aatccaatta 1080
 tcagaatcaa agacatgaac tttagcctc ttatcaatct tcgcagcctg gttatagctg 1140
 gtataaacct cacagaaaac ccagataacg ccttgggtgg actggaaaac ttagaaagca 1200
 tctctttta cgataacagg cttttaaaag taccctatgt tgcttctcaa aaagttgtaa 1260
 atctcaaatt ttggatcta aataaaaatc tattaaatag aatacgaagg ggtgatttta 1320
 gcaatgtct acacttaaaa gagttgggaa taaataatgc gcctgagctg atttccatcg 1380
 atagcttgc ttggataac ctgcaggat taagaaaaat agaagactact aacaacccta 1440
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 tgaacagcaa tgctctcagt gcccgttacc atggtaccat tgagtctctg ccaaacccta 1560
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<210> 69

<211> 708

<212> PRT

<213> Homo sapiens

<400> 69

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Thr	Thr	Leu	Val	Gln	Ala	Val	Asp	Lys	Lys	Val	Asp	Cys	Pro	Arg	Leu
				20				25				30			

Cys	Thr	Cys	Glu	Ile	Arg	Pro	Trp	Phe	Thr	Pro	Arg	Ser	Ile	Tyr	Met
				35			40					45			

Glu	Ala	Ser	Thr	Val	Asp	Cys	Asn	Asp	Leu	Gly	Leu	Leu	Thr	Phe	Pro
				50			55				60				

Ala	Arg	Leu	Pro	Ala	Asn	Thr	Gln	Ile	Leu	Leu	Gln	Thr	Asn	Asn
				65			70				75			80

Ile	Ala	Lys	Ile	Glu	Tyr	Ser	Thr	Asp	Phe	Pro	Val	Asn	Leu	Thr	Gly
				85				90					95		

Leu	Asp	Leu	Ser	Gln	Asn	Asn	Leu	Ser	Ser	Val	Thr	Asn	Ile	Asn	Val
				100				105				110			

Lys	Lys	Met	Pro	Gln	Leu	Leu	Ser	Val	Tyr	Leu	Glu	Glu	Asn	Lys	Leu
				115			120				125				

Thr	Glu	Leu	Pro	Glu	Lys	Cys	Leu	Ser	Glu	Leu	Ser	Asn	Leu	Gln	Glu
				130			135				140				

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
 225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
 260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
 275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
 290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
 305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
 325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly
 340 345 350

Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn
 355 360 365

Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr
 370 375 380

Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro
 385 390 395 400

Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met
 405 410 415

Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu
 420 425 430

Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala
 435 440 445

Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu
 450 455 460

Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
 465 470 475 480

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys
 485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys
 500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys
 515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser
 530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr
 545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys
 565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys
 580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn
 595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn
 610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
 625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
 645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
 660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
 675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
 690 695 700

Thr Asn Met Ser
 705

<210> 70
 <211> 1305
 <212> DNA
 <213> Homo sapiens

<400> 70
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 ttaccacgt tggatggat gatgaggaat gggctcgta ttatgtcgtc attccagcat 180
 gaatctggta gacctgtgtt taacccttgc cctctccatg tgcctccatc tacaaagttt 240
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 aattgccaac aacccttgc actgcgactg tactctacag caagttctga ggagcatggc 660
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ggtatattat	gtgaggcaaa	atcaggagga	tgcggaga	cacctcgaat	acttgaatc	900
cctgccaagc	aggcagaaga	aagcagatga	acctgatgat	attagcactg	tggtatagtg	960
tccaaactga	ctgtcattga	gaaagaaaga	aagtagtttgc	cgattgcagt	agaaataagt	1020
ggtttacttc	tcccatccat	tgtaaacatttgc	tgaaactttgc	tatttcagtttgc	tttttgaat	1080
tatgccactg	ctgaacttttgc	aacaaacacttgc	acaacataaaatgc	taattttgagt	ttaggtgatc	1140
caccccttaa	ttgtacccccc	gatgtatataatgc	ttctgagtaatgc	gctactatcttgc	gaacatttagt	1200
tagatccatc	tcactattatgc	ataatgaaatgc	ttatttttatgc	aattttaaag	caaataaaaag	1260
cttaactttgc	aaccatggatgc	aaaaaaaaaaaaaaatgc	aaaaaaaaaaaaaaatgc	aaaaaaaaaaaaaaatgc	aaaaaaaaaaaaaaatgc	1305

<210> 71

<211> 259

<212> PRT

<213> Homo sapiens

<400> 71

Met	Asn	Leu	Val	Asp	Leu	Trp	Leu	Thr	Arg	Ser	Leu	Ser	Met	Cys	Leu
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Leu	Leu	Gln	Ser	Phe	Val	Leu	Met	Ile	Leu	Cys	Phe	His	Ser	Ala	Ser
					20				25				30		

Met	Cys	Pro	Lys	Gly	Cys	Leu	Cys	Ser	Ser	Ser	Gly	Gly	Leu	Asn	Val
					35		40				45				

Thr	Cys	Ser	Asn	Ala	Asn	Leu	Lys	Glu	Ile	Pro	Arg	Asp	Leu	Pro	Pro
						50		55			60				

Glu	Thr	Val	Leu	Leu	Tyr	Leu	Asp	Ser	Asn	Gln	Ile	Thr	Ser	Ile	Pro
					65			70		75			80		

Asn	Glu	Ile	Phe	Lys	Asp	Leu	His	Gln	Leu	Arg	Val	Leu	Asn	Leu	Ser
					85			90			95				

Lys	Asn	Gly	Ile	Glu	Phe	Ile	Asp	Glu	His	Ala	Phe	Lys	Gly	Val	Ala
					100			105			110				

Glu	Thr	Leu	Gln	Thr	Leu	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Gln	Ser	Val
					115			120			125				

His	Lys	Asn	Ala	Phe	Asn	Asn	Leu	Lys	Ala	Arg	Ala	Arg	Ile	Ala	Asn
					130			135			140				

Asn	Pro	Trp	His	Cys	Asp	Cys	Thr	Leu	Gln	Gln	Val	Leu	Arg	Ser	Met
					145			150		155		160			

Ala	Ser	Asn	His	Glu	Thr	Ala	His	Asn	Val	Ile	Cys	Lys	Thr	Ser	Val
					165				170			175			

Leu	Asp	Glu	His	Ala	Gly	Arg	Pro	Phe	Leu	Asn	Ala	Ala	Asn	Asp	Ala
					180			185			190				

Asp	Leu	Cys	Asn	Leu	Pro	Lys	Lys	Thr	Thr	Asp	Tyr	Ala	Met	Leu	Val
					195			200			205				

Thr	Met	Phe	Gly	Trp	Phe	Thr	Met	Val	Ile	Ser	Tyr	Val	Val	Tyr	Tyr
					210			215			220				

Val	Arg	Gln	Asn	Gln	Glu	Asp	Ala	Arg	Arg	His	Leu	Glu	Tyr	Leu	Lys
					225			230			235			240	

Ser	Leu	Pro	Ser	Arg	Gln	Lys	Lys	Ala	Asp	Glu	Pro	Asp	Asp	Ile	Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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Thr Val Val

<210> 72

<211> 2290

<212> DNA

<213> Homo sapiens

<400> 72

accgagccga gcggaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
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 tgctgggctc agtgctgtca ggctcggcca cgggctgccc gccccctgc gagtgcctcg 180
 cccagggaccg cgctgtgctg tgccaccgca agtgctttgt ggcagtcggc gagggcatcc 240
 ccaccggagac ggcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
 agttcgcctg cttcccgcac ctggaggagc tggagctaa cgagaacatc gtgagcggcc 360
 tggagcccg cgccttcaac aacctttca acctccggac gctgggtctc cgagcaacc 420
 gcctgaagct catcccgcta ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
 tcagcgagaa caagatcggt atcctactgg actacatgtt tcaggacctg tacaaccta 540
 agtactgtt ggttggcgtc aatgacactcg tctacatctc tcaccggcgc ttcagcggcc 600
 tcaacagccg ggagcagctg acgctggaga aatgcaacct gacccatc cccaccgagg 660
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 aaaaaaaaaa 2290

<210> 73

<211> 620

<212> PRT

<213> Homo sapiens

<400> 73

Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
 1 5 10 15

Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
 20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
 35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
 50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
 65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
 85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
 100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
 115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
 130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
 145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
 165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
 180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
 195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
 210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
 225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
 245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
 260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
 275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
 290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
 305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
 325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
 340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
 355 360 365

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn
 580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
 610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 74

tcacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg

50

gg

52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77

ccatgtgtct cctcctacaa ag

22

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 78

ggaaatagat gtgatctgat tgg

23

<210> 79

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 79

cacctgttagc aatgcaaatc tcaaggaaat accttagagat cttcctcctg

50

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 80
agcaaccgccc tgaagctcat cc 22

<210> 81
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 81
aaggcgcggt gaaagatgta gacg 24

<210> 82
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 82
gactacatgt ttcaggacct gtacaacacctc aagtcaactgg aggttggcga 50

<210> 83
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 83
cccacgcgtc cgcacacctcg ccccgggctc cgaagcggct cgggggcgcc ctttcggta 60
acatcgtagt ccacccccc cccatccccca gccccgggg attcaggctc gccagcgccc 120
agccagggag cccgcggga agcgcgtatgg gggccccacgc cgctcgcctc ctgctccgtc 180
tcctgctgtt cgcctgctgc tgggcgcggc gccccggccaa cctctcccgag gacgacagcc 240
agccctggac atctgatgaa acatgtggtgg ctgttggcgc cgtgtgtctc aagtgcgaag 300
tgaagatca cgaggacta tccctgcaat ggtctaaaccct tgctcagcag actctctact 360
ttggggagaa gagagccccc cgagataatc gaattcagct ggttacccct acgccccacg 420
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acaagaagga atatccatc tagagggcgcc tgcccacttc ctgcggccccc cagggggccct 1380
gtggggactg ctggggccgt caccaccccg gacttgtaca gggcaaccgc agggccccc 1440
ctcccccttg ctccccagcc caccaccccc cctgtacaga atgtctgctt tgggtgcgg 1500
tttgtactcg gtttggaaatg gggagggagg agggcggggg gaggggaggg ttggccctcag 1560

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cccttccgt ggcttctctg catttgggtt attattattt ttgtaacaat cccaaatcaa 1620
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680
 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 85

gcttaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 86

aaccttggaaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 87

ccttagcacag tgacgaggga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 88
aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89
<211> 50
<212> DNA
<213> Artificial Sequence

<220> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 89
gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90
<211> 2755
<212> DNA
<213> Homo sapiens

<400> 90
gggggtttagg gaggaaggaa tccaccccca ccccccggaa ccctttctt ctcccttcct 60
ggcttcggac attggagcac taaatgaact tgaattgtgt ctgtggcagag caggatggtc 120
gctgttactt tgtatgaga tcggggatga attgctcgct ttaaaaatgc tgctttggat 180
tctgttgctg gagacgtctc tttgtttgc cgctggaaac gttacagggg acgtttgcaa 240
agagaagatc ttttcgtcga atgagataga agggggacta cacgtagact gtgaaaaaaaaa 300
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gacagtctgt gactttccctc actggcacaatggcccttac aacgcagatg gggcccacag 2220
agtgtatgac tggctctc actcgctctc agactaagac cccaaacccca ataggggagg 2280

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gcagagggaa ggcgatacat cttccac cgcaggcacc cgggggctg gagggggctg 2340
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 gcacaaccga aagggcctga ccccttaactt agctccctcc ttgaaacaaa gagcagactg 2460
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 atatctattt ttcccctgtg gattagcccc gtgatggctc cctgttggct acgcaggat 2700
 gggcagttgc acgaaggcat gaatgtattt taaaataagta actttgactt ctgac 2755

<210> 91

<211> 696

<212> PRT

<213> Homo sapiens

<400> 91

Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
 1 5 10 15

Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
 20 25 30

Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
 35 40 45

Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60

Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80

Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95

Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110

Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125

Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140

Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160

Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175

Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190

Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205

Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220

Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240

Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270
 Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285
 Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300
 Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320
 Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335
 Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350
 Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365
 Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380
 Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400
 Leu Ile Leu Leu Asp Leu Gly Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415
 Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430
 Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445
 Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460
 Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480
 Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495
 Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510
 Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525
 Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540
 Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560
 Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575
 Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr
660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
675 680 685

Cys Gly Ser His Ser Leu Ser Asp
690 695

<210> 92

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 92

gttggatctg ggcaacaata ac

22

<210> 93

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 93

attgttgtgc aggctgagtt taag

24

<210> 94

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 94

ggtggtata catggatagc aattacctgg acacgctgac ccggg

45

<210> 95

<211> 2226

<212> DNA

<213> Homo sapiens

<400> 95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

agtcgactgc	gtccccctgta	cccggcgcaca	gctgtgttcc	tgaccccaga	ataactcagg	60
gctgcaccgg	gcctggcagc	gctccgcaca	catttcctgt	cgcggcctaa	gggaaactgt	120
tggccgctgg	gccccgcgggg	ggattcttgg	cagttggggg	gtccgtcggg	agcgagggcg	180
gaggggaagg	gagggggaac	cggggttgggg	aagccagctg	tagagggcgg	tgaccgcgt	240
ccagacacag	ctctgcgtcc	tcgagcggga	cagatccaag	ttgggagcag	ctctgcgtgc	300
ggggcctcag	agaatgaggc	cgcggttcgc	cctgtgcctc	ctctggcagg	cgctctggcc	360
cgggcccggc	ggcggcgaac	accccactgc	cgaccgtgct	ggctgctcgg	cctcgggggc	420
ctgctacagc	ctgcaccacg	ctaccatgaa	gcggcaggcg	gccgaggagg	cctgcatccct	480
gcgagggtgg	gcgctcagca	ccgtgcgtgc	ggggcggcgg	ctgcgcgtg	tgctgcgtc	540
cctgcgggca	ggcccaggggc	ccggagggggg	ctccaaagac	ctgcgttct	gggtcgcact	600
ggagcgcagg	cgttcccact	gcacccttgg	gaacgaggct	ttgcggggtt	tctcctggct	660
gtcctccgac	cccggcggtc	tcgaaagcga	cacgctgcag	tgggtggagg	agccccaaacg	720
ctcctgcacc	gcccggagat	gcccgggtact	ccaggccacc	ggtgggggtcg	agcccgcagg	780
ctggaaaggag	atgcgatgcc	acctgcgcgc	caacggctac	ctgtgcaagt	accagttga	840
ggtcttgtt	cctgcgcgc	gccccggggc	cgccctctaac	tttagctatc	gcgcgcctt	900
ccagctgcac	agcgcgcgc	tggacttcag	tccacctggg	accgaggtga	gtgcgcctg	960
ccggggacag	ctcccgtatc	cagttacttg	catgcggac	gaaatcggcg	ctcgctggga	1020
caaactctcg	ggcgtgtgt	tgtgtccctg	ccccggggagg	tacccctgt	ctggcaaatg	1080
cgcagagctc	cctaactgccc	tagacgactt	gggaggctt	gcctgcgaat	gtgctacggg	1140
cttcgagctg	gggaaggacg	gccgctcttgc	tgtgaccagt	ggggaaaggac	agccgaccct	1200
tggggggacc	gggggtgccc	ccaggcgcgg	gccggccact	gcaaccagcc	ccgtgcccga	1260
gagaacatgg	ccaatcagg	tcgacgagaa	gctgggagag	acaccacttg	tccctgaaca	1320
agacaattca	gtAACATCTA	ttccctgagat	tcctcgatgg	ggatcacaga	gcacgatgtc	1380
tacccttcaa	atgtcccttc	aagccgagtc	aaaggccact	atcccccatt	cagggagcgt	1440
gatttccaa	ttaattcta	cgacttcctc	tgccactct	caggcttgc	actccctcctc	1500
tgccgtggc	ttcatatttgc	tgagcacagc	agtagtagt	ttggtgatct	tgaccatgac	1560
agtactgggg	tttgtcaagc	tctgtttca	cgaaagcccc	tcttcccagc	caaggaagga	1620
gtctatgggc	ccgcccggggc	tggagagtga	tcctgagccc	gctgtttgg	gctccagttc	1680
tgcacattgc	acaaaacaatg	gggtgaaagt	cggggactgt	gatctgcggg	acagagcaga	1740
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tgggcactcc	tgtgaacagt	tttctactt	tgtgaaacg	gggaaccaag	aggaacttac	1860
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aggagctaaa	tcagaactgc	acactccctc	cctgatgata	gaggaagtgg	aagtgcctt	1980
aggatggtga	tactggggg	ccgggttagt	ctggggagag	atattttctt	atgtttattc	2040
ggagaatttgc	gagaagtgtat	tgaactttc	aagacattgg	aaacaaatag	aacacaat	2100
aatttacatt	aaaaaataat	ttctacaaa	atggaaagga	aatgttctat	ttgttgcagg	2160
ctaggagtat	attggttcga	aatcccagg	aaaaaaataa	aaataaaaaaa	ttaaaggatt	2220
gttgc						2226

<210> 96

<211> 490

<212> PRT

<213> Homo sapiens

<400> 96

Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro

1

5

10

15

Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser

20

25

30

Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln

35

40

45

Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val

50

55

60

Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly

65

70

75

80

Pro Gly Pro Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu

85

90

95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
 100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
 115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
 130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
 145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
 165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
 180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
 195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
 210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
 225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
 245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
 260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
 275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
 290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
 305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
 325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
 340 345 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala
 355 360 365

Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr
 370 375 380

Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe
 385 390 395 400

Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr
 405 410 415

Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln
 420 425 430

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
435 440 445

Pro Ala Ala Leu Gly Ser Ser Ala His Cys Thr Asn Asn Gly Val
450 455 460

Lys Val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu
465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala
485 490

<210> 97

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 97

tggaaggaga tgcgatgcca cctg

24

<210> 98

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 98

tgaccagtgg ggaaggacag

20

<210> 99

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 99

acagagcaga gggtgccctt

20

<210> 100

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 100

tcagggacaa gtggtgtctc tccc

24

<210> 101

<211> 24

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 101

tcagggaaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 102

acagctcccg atctcagttt cttgcattcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

cgacgcgtg	ggattcagca	gtggcctgtg	gctgccagag	cagctcctca	ggggaaacta	60
agcgtcgagt	cagacggcac	cataatcgcc	tttaaaagtg	cctccgcct	gccggcccg	120
tatcccccg	ctacctggc	cgccccgcgg	cggtgcgcgc	gtgagaggga	gcgcgcgggc	180
agccgagcgc	cggtgtgagc	cagcgctgct	gccagtgtga	gcggcggtgt	gagcgcgggtg	240
ggtgcggagg	ggcgtgtgt	ccggcgcgcg	cgccgtgggg	tgcaaacc	gagcgtctac	300
gctgccatga	ggggcgcgaa	cgcctggcg	ccactctgcc	tgctgtggc	tgccgcacc	360
cagctctcg	ggcagcagtc	cccagagaga	cctgtttca	catgtgg	cattctact	420
ggagagtctg	gatttatttg	cagtgaaggt	tttccctggag	tgtaccctcc	aaatagcaaa	480
tgtacttgg	aaatcacagt	tcccaagga	aaagttagtgc	ttctcaattt	ccgattcata	540
gacctcgaga	gtgacaacct	gtgccgctat	gactttgtgg	atgtgtacaa	tggccatgcc	600
aatggccagc	gcattggccg	cttctgtggc	actttccggc	ctggagccct	tgtgtccagt	660
ggcaacaaga	tgatggtgc	gatgatttct	gatgccaaca	cagctggcaa	tggcttcatg	720
gccatgttct	ccgctgctg	accaaacgaa	agaggggatc	agtattgtgg	aggactcc	780
gacagaccc	ccggctctt	taaaaccccc	aactggccag	accgggatta	ccctgcagga	840
gtcacttgc	tgtggcacat	tgtggcacat	aagaatcgc	ttatagaatt	aaagtttgc	900
aagtttgc	tggagcgaga	taactactcg	cgatatttgc	atgtggctgt	gtttaatggc	960
ggggaaagtca	acgatgtcg	aagaatttgc	aagtatttgc	gtgatagtcc	acctgcgcca	1020
atttgtctg	agagaaatgc	acttcttatt	cagttttat	cagatcttgc	ttaactgc	1080
gatgggtta	ttggtcacta	catattcagg	ccaaaaaaac	tgcctacaac	tacagaacag	1140
cctgtcacca	ccacattccc	tgtaaccacg	ggtttttttt	ccaccgtggc	tttgtgtcaa	1200
caaaagtgt	gacggacggg	gactctggag	ggcaattatt	gttcaagtgc	ctttgttata	1260
gccggcactg	ttatcacaac	catcaactgc	gatggggat	tgcacgccc	agtctcgatc	1320
atcaacatct	acaaagaggg	aaatttgcg	attcagcagg	cgggcaagaa	catgagtgcc	1380
aggctactg	tcgtctgc	gcagtgcct	ctcctcagaa	gaggctaaa	ttacattatt	1440
atggccaag	taggtgaaga	tggcgaggc	aaaatcatgc	caaacacgtt	tatcatgtat	1500
ttcaagacca	agaatcgaaa	gctccctggat	gccttttttt	ataagcaatg	ttaacagtga	1560
acttgtcca	ttaagctgt	attctgcct	tgccttttgc	agatctatgt	tctctcaga	1620
aaaaaaaaaa	tacttataaa	attacatatt	ctgaaagagg	attccgaaag	atgggactgg	1680
ttgacttcc	acatgtatgg	ggtatggaggc	ctccgagata	gctgaggaa	gttcttgcc	1740
tgctgtcaga	ggagcagct	tctgatttgc	aacctgcgc	cttagtgcgg	tgataggaag	1800
ctaaaagtgt	caagcgttgc	cagcttggaa	gcgtttttt	atacatctc	gtaaaaggat	1860
attttagaat	tgatgtgt	gaagatgtca	aaaaaaagg	ttagaagtgc	aatatttata	1920
gtgttatttgc	tttcaccttc	aaggccttgc	cctgagggt	tacaatcttgc	tcttcgttt	1980
tctaaatcaa	tgcttaataaa	aatatttttgc	aaggaaaaaaa	aaaaaaa		2026

<210> 104

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 415
<212> PRT
<213> Homo sapiens

<400> 104
Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Ala Ala
1 5 10 15
Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
20 25 30
Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
35 40 45
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
50 55 60
Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
65 70 75 80
Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
85 90 95
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
100 105 110
Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
115 120 125
Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
130 135 140
Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
145 150 155 160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
165 170 175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
180 185 190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
195 200 205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
210 215 220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
225 230 235 240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
245 250 255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
260 265 270
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
275 280 285
Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
290 295 300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305 310 315 320

Thr Val Ile Thr Thr Ile Thr Arg Asp Gly Ser Leu His Ala Thr Val
325 330 335Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala
340 345 350Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
355 360 365Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
370 375 380Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
385 390 395 400Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt 22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac 22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgt tctgt 45

<210> 108

<211> 1838

<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tggcgccccc acggcgcccc cgggctgggg cggtcgccttc 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ttcctctcc gtggcctacg agggccccca gcctggtaa agatggcccc atggcccccg 120
 aaggcctag tcccagctgt gctctgggc ctcagccct tcctcaacct cccaggacct 180
 atctgctcc agccctctcc acctccccag tcttctcccc cgcctcagcc ccatccgtgt 240
 cataacctgcc ggggactgt tgacagctt aacaagggcc tggagagaac catccggac 300
 aacttggag gtggaaacac tgcctggag gaagagaatt tgccaataa caaagacagt 360
 gagaccgcgcc tggtagaggt gctggagggt gtgtcagca agtcagactt cgagtgcac 420
 cgcctgctgg agctgatgt ggagctggg gagagctgtt gtttcaaaa gcagcaggag 480
 gccccggacc tcttccatgt gctgtctca gattccctga agctctgtc ccccgccagg 540
 accttcgggc ccttcgtc tccctgtc gggggaaacag agaggccctg cgggtggctac 600
 gggcaatgtg aaggagaagg gacacgaggg ggcagcgggc actgtactg ccaagccggc 660
 tacgggggtg aggccctgtgg ccagtgtggc ttggctact ttgaggcaga acgcaacgcc 720
 agccatctgg tatgttcggc ttgtttggc ccctgtgcc gatgctcagg acctgaggaa 780
 tcaaactgtt tgcaatgcaa gaagggtctgg gcccctgc acctcaagtg tgttagacatt 840
 gatgagtgtg gcacagaggg agccaaactgt ggagctgacc aattctgcgt gaacacttag 900
 ggctccatg agtgcgaga ctgtccaaag gcctgcctag gtcgcattgg ggcaggggcca 960
 ggtcgcgtga agaagtgttag ccctggctat cagcagggtt gctccaagtg tctcgatgtg 1020
 gatgagtgtg agacagaggt gtgtccggg gagaacaagc agtgtaaaaa caccgaggag 1080
 gtttatcgct gcatctgtc cgagggtctac aagcagatgg aaggcatctg tgtgaaggag 1140
 cagatcccg agtcagcagg cttcttcata gagatgacag aagacgagtt ggtggctgt 1200
 cagcagatgt tcttggcat catcatctgt gcaactggca cgctggctgc taagggcgac 1260
 ttgggttca cgcgcattt cattgggct gtggcggca tgactggcta ctgggtgtca 1320
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 gtaggacctc ctcccaccca cgctggccccc agagcttggg ctggccctct gctggacact 1440
 caggacagct tggtttattt ttgagagtgg gtaagcacc cctacctgccc ttacagagca 1500
 gcccaggatcc ccaggccccg gcagacaagg cccctgggtt aaaaagtgc cctgaaggag 1560
 gataccatga gctcttcacc tggcggggac tggcaggctt cacaatgtgt gaatttcaaa 1620
 agttttccct taatgggtgc tgctagatgt ttggccctg ctttaggatta ggtggtcctc 1680
 acaggggtgg ggcacatcaca gctccctcct gccagctca tgctgccagt tcctgttctg 1740
 tggcaccac atccccacac cccattgcca cttatttattt catctcagga aataaagaaaa 1800
 ggtcttggaa agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1838

<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met	Ala	Pro	Trp	Pro	Pro	Lys	Gly	Leu	Val	Pro	Ala	Val	Leu	Trp	Gly
1															15

Leu	Ser	Leu	Phe	Leu	Asn	Leu	Pro	Gly	Pro	Ile	Trp	Leu	Gln	Pro	Ser
															20
															25
															30

Pro	Pro	Pro	Gln	Ser	Ser	Pro	Pro	Pro	Gln	Pro	His	Pro	Cys	His	Thr
															35
															40
															45

Cys	Arg	Gly	Leu	Val	Asp	Ser	Phe	Asn	Lys	Gly	Leu	Glu	Arg	Thr	Ile
															50
															55
															60

Arg	Asp	Asn	Phe	Gly	Gly	Asn	Thr	Ala	Trp	Glu	Glu	Glu	Asn	Leu	
															65
															70
															75

Ser	Lys	Tyr	Lys	Asp	Ser	Glu	Thr	Arg	Leu	Val	Glu	Val	Leu	Glu	Gly
															85
															90
															95

Val	Cys	Ser	Lys	Ser	Asp	Phe	Glu	Cys	His	Arg	Leu	Leu	Glu	Leu	Ser
															100
															105
															110

Glu	Glu	Leu	Val	Glu	Ser	Trp	Trp	Phe	His	Lys	Gln	Gln	Glu	Ala	Pro
															115
															120
															125

Asp	Leu	Phe	Gln	Trp	Leu	Cys	Ser	Asp	Ser	Leu	Lys	Leu	Cys	Cys	Pro
															130
															135
															140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
355 360 365

Met Phe Phe Gly Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
405 410 415

Ile Lys Gly Arg
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 110						
cctggctatc	agcaggtggg	ctccaagtgt	ctcgatgtgg	atgagtgtga	50	
<210> 111						
<211> 22						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> Description of Artificial Sequence: Synthetic						
oligonucleotide probe						
<400> 111						
attctgcgtg	aacactgagg	gc			22	
<210> 112						
<211> 22						
<212> DNA						
<213> Artificial Sequence						
<220>						
<223> Description of Artificial Sequence: Synthetic						
oligonucleotide probe						
<400> 112						
atctgcttgt	agccctcggc	ac			22	
<210> 113						
<211> 1616						
<212> DNA						
<213> Homo sapiens						
<220>						
<221> modified_base						
<222> (1461)..(1461)						
<223> a, t, c or g						
<400> 113						
tgagaccctc	ctgcagcctt	ctcaaggac	agccccactc	tgccttgc	tcctccaggg	60
cagcaccatg	cagccctgt	ggctctgt	ggcaactctgg	gtgttgc	tggccagccc	120
cggggccgcc	ctgaccgggg	agcagctcct	gggcagcctg	ctggggcagc	tgcagctcaa	180
agaggtgccc	accctggaca	gggcgcacat	ggaggagctg	gtcatccca	cccacgttag	240
ggcccaagtac	gtggccctgc	tgcagcgcag	ccacggggac	cgctcccg	aaaagagggt	300
cagccagacg	ttccgagagg	ttgcggcag	gttcctggcg	ttggaggcca	gcacacac	360
gctgggttgc	ggcatggacg	agcgctgccc	gccccaaacgc	gagctgggtgc	aggccgtgct	420
gcggcttcc	caggagccgg	tcccaaggc	cgcgtgcac	aggcacgggc	ggctgtcccc	480
gcccacgcgc	cgggcccccgg	tgaccgtcga	gtggctgcgc	gtccgcgacg	acggctccaa	540
ccgcacctcc	ctcatcgact	ccaggtgggt	gtccgtccac	gagagcggct	ggaaggccctt	600
cgacgtgacc	gaggccgtga	acttctggca	gcagctgagc	cgccccccggc	agccgctgct	660
gctacaggtg	tcggtgac	gggagcatct	ggggccgtg	gcgtccggcg	cccacaagct	720
ggccgcctt	gcctcgac	gggcgcacg	cgggcttgg	gagcccccagc	tggagctgca	780
cacccctggac	tttggggact	atggagctca	ggggcactgt	gaccctgaag	caccaatgac	840
cgagggcacc	cgctgctgcc	gccaggagat	gtacattgac	ctgcagggga	tgaagtggc	900
cgagaactgg	gtgctggagc	ccccgggctt	cctggcttat	gagtgtgtgg	gcacctgccc	960
gcagccccc	gaggccctgg	ccttcgaatg	gccgttctg	gggcctcgac	agtgcacatcgc	1020
ctcgagact	gactcgctgc	ccatgatcg	cagcatcaag	gaggaggc	ggaccaggcc	1080
ccaggtggtc	agcctgccc	acatgagggt	gcagaagtgc	agctgtgcct	cggatgggtgc	1140
gctcgccca	aggaggctcc	agccataggc	gccttagtgc	gccatcgagg	gacttgactt	1200
gtgtgtgttt	ctgaagtgtt	cgagggtacc	aggagagctg	gcatgactg	aactgctgat	1260
ggacaaatgc	tctgtgtct	ctagtgagcc	ctgaatttgc	ttccctgtac	aagttacctc	1320
acctaatttt	tgcttctcag	gaatgagaat	cttggccac	tggagagccc	ttgctcagtt	1380
ttctctattc	ttattattca	ctgcactata	ttctaaagcac	ttacatgtgg	agataactgt	1440

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
 aaagtccctcc accaccactc tggacctaag acctggggtt aagtgtgggt tgtgcacccc 1560
 caatccagat aataaagact ttgtaaaaca tgaataaaac acattttatt ctaaaa 1616

<210> 114

<211> 366

<212> PRT

<213> Homo sapiens

<400> 114

Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
 1 5 10 15

Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
 245 250 255

Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
 260 265 270

Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 115

aggactgcca taacttgccct g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtccctt cggccgctgt tgggtcagtgc gcctgatcgc gatggggaca 60

aaggcgcaag tcgagaggaa actgttgc ctcttcataat tggcgatcct gttgtgtcc 120

ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcaaat tcctgagaat 180

aatcctgtga agttgtcctg tgcctactcg ggctttctt ctccccgtgt ggagtggaaag 240

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tttgaccaag gagacaccac cagactcggt tgctataata acaagatcac agcttcctat 300
 gaggaccggg tgaccttctt gccaactggt atcaccttca agtccgtgac acgggaagac 360
 actgggacat acacttgat ggtctctgag gaaggcgca acagctatgg ggaggtcaag 420
 gtcaagctca tcgtgcttgt gcctccatcc aagcctacag ttaacatccc ctcccttgcc 480
 accatggga accggcagt gctgacatgc tcagaacaag atggttcccc accttctgaa 540
 tacaccttgt tcaaagatgg gatagtatg cctacgaatc ccaaaggac ccgtgccttc 600
 agcaactt cctatgtctt gaatcccaca acaggagagc tggctttga tccccctgtca 660
 gcctctgata ctggagaata cagctgtgag gcacggaaatg ggtatggac acccatgact 720
 tcaaattgtg tgccatggag agctgtggag cggatgtgg gggatcatgt ggcagccgtc 780
 cttgttaaccctt tgattctcctt gggatcttgc ttttttgca tctgggttgc ctatagccga 840
 ggccactttt gacagaacaaa gaaaggact tcgagaatg aggtattta cagccagcct 900
 agtgcccggaa gtgaaggaga attcaaacag acctcgatcat tcctgggttg agcctggatcg 960
 gctaccggcc tatcatctgc atttgcctta ctcaggtgtc accggactctt ggccccctgat 1020
 gtctgttagtt tcacaggatg ctttattttgtt cttctacacc ccacaggggcc ccctacttct 1080
 tcggatgtgt ttttaataat gtcaatgtatg tgcccccattcc tccttcatgc cctccctcc 1140
 tttccatcca ctgctgatgt gccttggaaat ttttttttttttgc catttctttg 1200
 agggatcagg aaggaatcctt gggatgtgcca ttgacttccc ttctaagtag acagcaaaaa 1260
 tggcgggggtt cgcaggaaatc tgcaactcaac tgcccacccgt gctggcaggg atctttgtat 1320
 aggtatcttg agcttggatc tgggtctttt ccttgtgtac tgacgaccag ggccagctgt 1380
 tctagagcgg gaatttagagg cttagcgcc tgaaatgtt gtttttttttttgc gacactgggg 1440
 tccttccatcc tctggggccc actctttctt gtcttccat gggaaatgtgccc actggatcc 1500
 ctctccctgtt ccctccctgaa tacaagctga ctgacattga ctgtgtctgtt ggaaaatggg 1560
 agctttgtt gtggagagca tagtaaattttt tcagagaact tgaagccaaa aggatttaaaa 1620
 accgctgctc taaagaaaag aaaactggag gctggcgca gtggctcactg cctgtatcc 1680
 cagaggctga ggcaggcgga tcacctgagg tcgggagttc gggatcagcc tgaccaacat 1740
 ggagaaaccc tactggaaat acaaagtttgc ccaggcatgg tggtgcatgc ctgttagtccc 1800
 agctgcttag gaggctggca acaagagcaa aactccagct caaaaaaaaaaaaaaaa 1857

<210> 119

<211> 299

<212> PRT

<213> Homo sapiens

<400> 119

Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15

Leu Ala Ile Leu Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30

Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45

Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Gly Ile Leu Val Phe Gly
245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctgtt tccc

24

<210> 121

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 121

tgatcgcgat ggggacaaaag gcgcaagctc gagagggaaac tgggtgtgcct

50

<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 122

acacacctgggtt caaagatggg

20

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 123
taggaagagt tgctgaaggc acgg 24

<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 124
ttgccttact caggtgctac 20

<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 125
actcagcagt ggttaggaaag 20

<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 126
cagcgcgtgg ccggcgccgc tgtggggaca gcatgagcgg cggttggatg ggcgcaggttg 60
gagcgtggcg aacaggggct ctgggcctgg cgctgctgct gctgctcggc ctcggactag 120
gcctggaggc cgccgcgagc ccgcatttcca ccccgaccctc tgcccaggcc gcaggccccca 180
gctcaggctc gtgcccaccc accaagttcc agtgcgcac cagtggttta tgcgtcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgc 300
ggatttggcc atgtacccag aaaggggcaat gcccaccgc cccctggcctc ccctgcccc 360
gcacccggcgt cagtgactgc tctggggaa ctgacaagaa actgcgcac tgcagccg 420
tggcttcctt agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tggaaacca 540
atgagatcct cccggaaagg gatgccacaa ccatggggcc ccctgtgacc ctggagagt 600
tcacccctctt caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccc 660
ctgtcgggaa tggccacatcc tcctctgccc gagaccagtc tggaaaccca actgcctatg 720
gggttattgc agctgctgcg gtgctcagtg caagcctgtt caccgcacc ctcctcctt 780
tgtccctggct ccgagcccgag gagcgcctcc gcccacttgg gttacttgg gccatgaagg 840
agtccctgtc gctgtcagaa cagaagaccc cgctgcccctg aggacaagca cttgccacca 900
ccgtcactca gcccggccg tagccggaca ggaggagac agtgatgcgg atgggtaccc 960
gggcacacca gcccctcagag acctgagttc ttctggccac gtgaaacctc gaacccgagc 1020
tcctgcagaa gtggccctgg agattgaggg tccctggaca ctccctatgg agatccgggg 1080
agcttagatg gggAACCTGC cacagccaga actgaggggc tggcccccagg cagctcccag 1140
gggtagaaac gcccctgtgc ttaagacact ccctgctgccc cctgtgagg gtggcgattt 1200

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
aagttgcttc 1210

<210> 127

<211> 282

<212> PRT

<213> Homo sapiens

<400> 127

Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
1 5 10 15

Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
20 25 30

Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
35 40 45

Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
50 55 60

Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
65 70 75 80

Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
85 90 95

Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Ser Trp Leu Arg Ala Gln
245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
275 280

<210> 128

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 129

ttggttccac agccgagctc gtcg

24

<210> 130

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 130

gaggaggagt gcaggattga gccatgtacc cagaaaggc aatgccacc

50

<210> 131

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (1837)..(1837)

<223> a, t, c or g

<400> 131

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gggttagact	ggcgggggga	ggaggcggag	gagggaagga	agctgcattgc	atgagaccca	120
cagactcttg	caagctggat	gccctctgtg	gatgaaagat	gtatcatgga	atgaacccga	180
gcaatggaga	tggatttcta	gagcagcagc	agcagcagca	gcaacctcg	tccccccaga	240
gactcttggc	cgtgatcctg	tggtttcagc	tggcgctgtg	cttcggccct	gcacagctca	300
cggccgggtt	cgtgacccctt	caagtgtgt	ctgaccccg	cattcccgag	aatggcttca	360
ggaccccccag	cggagggggtt	ttctttgaag	gctctgtgc	ccgatttcac	tgccaagacg	420
gattcaagct	gaagggcgt	acaagagac	tgtgtttgaa	gcattttaat	ggaaccctag	480
gctggatccc	aagtgataat	tccatctgtg	tgcaagaaga	ttggcgatc	cctcaaatcg	540
aagatgctga	gattcataac	aagacatata	gacatggaga	gaagctaatc	atcacttgc	600
atgaaggatt	caagatccgg	taccccgacc	tacacaatat	ggtttcatta	tgtcgcgatg	660
atggAACGTG	gaataatctg	cccatctgtc	aaggctgcct	gagacctcta	gcctcttcta	720
atggctatgt	aaacatctct	gagctccaga	cctccctccc	ggtggggact	gtgatctcct	780
atcgctgtt	tcccgattt	aaacttgcgt	ggtctgcgt	tcttgatgc	ttacaaaacc	840
ttatctggtc	gtccagccca	ccccggtgcc	ttgctctgga	agccaaatgc	tgtccactac	900
ctccaatggt	gagtacacgga	gatttcgtct	gccaccccg	gccttgcgag	cgctacaacc	960
acggaactgt	ggtggagttt	tactgcgatc	ctggctacag	cctcaccagc	gactacaagt	1020

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acatcacctg ccagtatgga gagtggttgc cttcttatca agtctactgc atcaaatcag 1080
 agcaaacgtg gcccagcacc catgagaccc tcctgaccac gtgaaagatt gtggcgttca 1140
 cggcaaccag tggctgctg gtgctgctgc tcgtcatcct ggcaggatg ttccagacca 1200
 agttcaaggc ccacttccc cccagggggc ctccccggag ttccagcagt gaccctgact 1260
 ttgtgtgtt agacggcgtg cccgtcatgc tcccgtctta tgacgaagct gtgagtgccg 1320
 gcttgagtgc ctttaggcccc gggatcatgg cctctgtggg ccaggcgtgc cccttacccg 1380
 tggacacca gagcccccca gcataccccc gctcaggaga cacggacaca gcccagggg 1440
 agtcgaaac ctgtgacagc gtctcaggct cttctgagct gctccaaagt ctgtattcac 1500
 ctccccagggtg ccaagagagc acccacccctg ctccggacaa cccgtacata attgcccac 1560
 cggcagagga ggtggcattcc accagcccg gcatccatca tgcccaactgg gtgtgttcc 1620
 taagaaactg aatgattaaa aaatttccca aagtgtcctg aagtgtctct tcaaatacat 1680
 gttgatctgt ggagttgatt ccttccttc tcttggtttt agacaaatgt aaacaaagct 1740
 ctgatccctt aaattgctat gctgatagag tggtgaggcc tggaaagctt atcaagtcct 1800
 gttttttttt gacacagact gattaaaaat taaaagnaaa aaa 1843

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met	Tyr	His	Gly	Met	Asn	Pro	Ser	Asn	Gly	Asp	Gly	Phe	Leu	Glu	Gln
1				5				10					15		

Gln	Gln	Gln	Gln	Gln	Pro	Gln	Ser	Pro	Gln	Arg	Leu	Leu	Ala	Val
20					25				30					

Ile	Leu	Trp	Phe	Gln	Leu	Ala	Leu	Cys	Phe	Gly	Pro	Ala	Gln	Leu	Thr
35				40					45						

Gly	Gly	Phe	Asp	Asp	Leu	Gln	Val	Cys	Ala	Asp	Pro	Gly	Ile	Pro	Glu
50					55				60						

Asn	Gly	Phe	Arg	Thr	Pro	Ser	Gly	Gly	Val	Phe	Phe	Glu	Gly	Ser	Val
65				70					75			80			

Ala	Arg	Phe	His	Cys	Gln	Asp	Gly	Phe	Lys	Leu	Lys	Gly	Ala	Thr	Lys
85					90				95						

Arg	Leu	Cys	Leu	Lys	His	Phe	Asn	Gly	Thr	Leu	Gly	Trp	Ile	Pro	Ser
100					105				110						

Asp	Asn	Ser	Ile	Cys	Val	Gln	Glu	Asp	Cys	Arg	Ile	Pro	Gln	Ile	Glu
115					120				125						

Asp	Ala	Glu	Ile	His	Asn	Lys	Thr	Tyr	Arg	His	Gly	Glu	Lys	Leu	Ile
130					135				140						

Ile	Thr	Cys	His	Glu	Gly	Phe	Lys	Ile	Arg	Tyr	Pro	Asp	Leu	His	Asn
145				150				155					160		

Met	Val	Ser	Leu	Cys	Arg	Asp	Asp	Gly	Thr	Trp	Asn	Asn	Leu	Pro	Ile
165					170				175						

Cys	Gln	Gly	Cys	Leu	Arg	Pro	Leu	Ala	Ser	Ser	Asn	Gly	Tyr	Val	Asn
180					185				190						

Ile	Ser	Glu	Leu	Gln	Thr	Ser	Phe	Pro	Val	Gly	Thr	Val	Ile	Ser	Tyr
195					200				205						

Arg	Cys	Phe	Pro	Gly	Phe	Lys	Leu	Asp	Gly	Ser	Ala	Tyr	Leu	Glu	Cys
210					215				220						

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu
 225 230 235 240

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe
 245 250 255

Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val
 260 265 270

Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr
 275 280 285

Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys
 290 295 300

Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr
 305 310 315 320

Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu
 325 330 335

Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His
 340 345 350

Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe
 355 360 365

Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala
 370 375 380

Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val
 385 390 395 400

Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr
 405 410 415

Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys
 420 425 430

Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro
 435 440 445

Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile
 450 455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgcttcc cg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 134

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 134

agccaggatc gcagtaaaac tcc

23

<210> 135

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 135

atttaaacctt gatgggtctg cgtatcttga gtgcttacaa aaccttatct

50

<210> 136

<211> 1815

<212> DNA

<213> Homo sapiens

<400> 136

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ccgttagcgc	cgagtgtcg	ggggcgcacc	cgagtcggc	catgaggccg	gaaaccgcgc	180
tacaggccgt	gctgctggcc	gtgctgctgg	tggggctgcg	ggccgcgacg	gtcgccctgc	240
tgagtgcc	ggatttggac	ctcagaggag	ggcagccagt	ctgcccggg	gggacacaga	300
ggcctgtt	taaagtattt	tactccatg	atacttctcg	aagactgaac	tttgaggaaag	360
ccaaagaagc	ctgcaggagg	gatggaggcc	agctagtcg	catcgagtct	gaagatgaac	420
agaaaactgt	agaaaaagttc	attaaaaacc	tcttgcac	tgtatggtac	ttctggattg	480
ggctcaggag	gcgtgaggag	aaacaaagca	atagcacagc	ctgcccaggac	ctttatgtct	540
ggactgatgg	cagcatatca	caatttagga	actggatgt	ggatgagccg	tcctgcggca	600
gcgagggtctg	cgtggtcatg	taccatcagc	catcggcacc	cgttggcattc	ggaggccct	660
acatgttcca	gttggatgt	gaccggtgca	acatgaagaa	caatttattt	tgcaaataatt	720
ctgatgagaa	accaggatc	ccttttagag	aagctgaagg	tgaggaaaca	gagctgacaa	780
cacctgtact	tccagaagaa	acacaggaa	aagatgc	aaaaacattt	aaagaaaagta	840
gagaagctgc	tttgaatctg	gcctcatcc	taatccccag	cattttccctt	ctcctcctcc	900
ttgtggtcac	cacagttgt	tgttgggtt	ggatctgtag	aaaaagaaaa	cgggagcagc	960
cagaccctag	cacaaagaag	caacacacca	tctggccctc	tcctcaccag	ggaaacagcc	1020
cgaccctaga	ggtctacaat	gtcataagaa	aacaaagcg	agctgactta	gctgagaccc	1080
ggccagac	gaagaatatt	tcattccgag	tgtgttccgg	agaagccact	cccgatgaca	1140
tgtctgtt	ctatgacaac	atggctgtga	acccatcaga	aagtgggtt	gtgactctgg	1200
tgagcgttga	gagtggattt	gtgaccaatg	acatttatga	gttctccca	gaccaaata	1260
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aaactgaaac	tgacaacaat	ggaaaagaaa	tgataagca	aatcccttta	ttttctataa	1380
ggaaaataca	cagaagggtct	atgaacaagc	ttagatcagg	tcctgtggat	gagcatgtgg	1440
tccccacgac	ctccctgttgg	accccacgt	tttggctgt	tcctttatcc	cagccagtca	1500
tccagctcg	ccttatgaga	aggtacctt	cccaggctg	gcacatagta	gagtctcaat	1560
aaatgtcact	tgggtgggtt	tatctaactt	ttaaggac	gagctttacc	tggcagtgtat	1620
aaagatgggc	tgtggagctt	ggaaaaccac	ctctgtttt	cttgccttat	acagcagcac	1680
atattatcat	acagacagaa	aatccagaat	cttttcaag	cccacatag	gtagcacagg	1740
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agcaggaaaa	aaaaaa					1815

<210> 137

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 382
<212> PRT
<213> Homo sapiens

<400> 137
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1 5 10 15
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
20 25 30
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
35 40 45
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
50 55 60
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
65 70 75 80
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
85 90 95
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
100 105 110
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
115 120 125
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
130 135 140
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
145 150 155 160
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
165 170 175
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
180 185 190
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
195 200 205
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
210 215 220
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
225 230 235 240
Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
245 250 255
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
260 265 270
Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
275 280 285
Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
290 295 300
Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
325 330 335Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
340 345 350Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
355 360 365Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
370 375 380

<210> 138

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 138

gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50.

<210> 139

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 139

aagccaaaga agcctgcagg aggg 24

<210> 140

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 140

cagtccaagc ataaaggtcc tggc 24

<210> 141

<211> 1514

<212> DNA

<213> Homo sapiens

<400> 141

ggggtctccc tcagggccgg gaggcacagc ggtccctgct tgctgaaggg ctggatgtac 60

gcatccgcag gttcccgccg acttgggggc gccccgctgag ccccccgcgc cgcagaagac 120

ttgtgtttgc ctccctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180

tggtgtttc agcatgcgcg tttggacccc aatgggcgtc ctgcacccgc tggcgtactg 240

cctgcaccag cggcggtgg ccctggccga gctgcaggag gccgatggcc aatgtccgg 300

cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcggt tttcgacacg gggctcgag 360

tcctctcaag ccgctccgc tggaggagca ggttagagtgg aaccccccagc tattagaggt 420

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gctgaccaag	gtgggcattgc	agcaaatgtt	tgccttggga	gagagactga	ggaagaacta	600
tgtggaaagac	attcccttc	tttcaccaac	cttcaaccca	caggaggtct	ttattcggtc	660
cactaacatt	tttcggaaatc	tggagtcac	ccgttggttt	ctggctggc	ttttccagtg	720
tcagaaagaa	gacccatca	tcatccacac	tcatgaagca	gattcagaag	tcttgatcc	780
caactaccaa	agctgctgga	gcctgaggca	gagaaccaga	ggccggaggc	agactgcctc	840
ttagcagcca	gaaatctcag	aggattgaa	aaagggtgaag	gacaggatgg	gcattgacag	900
tagtgataaa	gtggacttc	tcatccct	ggacaacatg	gctggccgac	aggcacacaa	960
cctcccaagc	tgccccatgc	tgaagagatt	tgcacggatg	atcaacaga	gagctgtgga	1020
cacatccctg	tacatactgc	ccaaggaaga	caggaaagt	cttcagatgg	cagttaggccc	1080
attccctccac	atcctagaga	gcaacctgct	gaaagccatg	gactctgcca	ctgccccca	1140
caagatcaga	aagctgtatc	tctatgcggc	tcatgtgtg	accttcatac	cgctcttaat	1200
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agtttatacc	ttaagccag	aaaaatacca	tgcactctgc	tctcaaactc	aggtgatgga	1440
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gccttatac	aatg					1514

<210> 142

<211> 428

<212> PRT

<213> Homo sapiens

<400> 142

Met	Ile	Thr	Gly	Val	Phe	Ser	Met	Arg	Leu	Trp	Thr	Pro	Val	Gly	Val
1				5					10					15	

Leu	Thr	Ser	Leu	Ala	Tyr	Cys	Leu	His	Gln	Arg	Arg	Val	Ala	Leu	Ala
								20				25		30	

Glu	Leu	Gln	Glu	Ala	Asp	Gly	Gln	Cys	Pro	Val	Asp	Arg	Ser	Leu	Leu
							35		40			45			

Lys	Leu	Lys	Met	Val	Gln	Val	Val	Phe	Arg	His	Gly	Ala	Arg	Ser	Pro
							50		55			60			

Leu	Lys	Pro	Leu	Pro	Leu	Glu	Glu	Gln	Val	Glu	Trp	Asn	Pro	Gln	Leu
							65		70		75		80		

Leu	Glu	Val	Pro	Pro	Gln	Thr	Gln	Phe	Asp	Tyr	Thr	Val	Thr	Asn	Leu
							85		90			95			

Ala	Gly	Gly	Pro	Lys	Pro	Tyr	Ser	Pro	Tyr	Asp	Ser	Gln	Tyr	His	Glu
							100		105			110			

Thr	Thr	Leu	Lys	Gly	Gly	Met	Phe	Ala	Gly	Gln	Leu	Thr	Lys	Val	Gly
						115		120			125				

Met	Gln	Gln	Met	Phe	Ala	Leu	Gly	Glu	Arg	Leu	Arg	Lys	Asn	Tyr	Val
						130		135			140				

Glu	Asp	Ile	Pro	Phe	Leu	Ser	Pro	Thr	Phe	Asn	Pro	Gln	Glu	Val	Phe
						145		150			155		160		

Ile	Arg	Ser	Thr	Asn	Ile	Phe	Arg	Asn	Leu	Glu	Ser	Thr	Arg	Cys	Leu
						165		170			175				

Leu	Ala	Gly	Leu	Phe	Gln	Cys	Gln	Lys	Glu	Gly	Pro	Ile	Ile	Ile	His
						180		185			190				

Thr	Asp	Glu	Ala	Asp	Ser	Glu	Val	Leu	Tyr	Pro	Asn	Tyr	Gln	Ser	Cys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
195 200 205

Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Page 71

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga 24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttccgt ggtaatagag ctgc 24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctcttacag ccagg 45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctttaa catacttgca gctaaaacta aatattgctg cttgggacc tccttctagc 60
cttaaatttc agctcatcac cttcacctgc cttggatcatg gctctgctat tctccttgat 120
ccttgcatt tgcaccagac ctggattcct agcgtctcca tctggagtgc ggctgggtgg 180
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caaccatgtatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gacttagg 840
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ggtgggcattc atctaattctg ttgagtgccct gaatagaaga aaaacacaga agaaggggagc 1200
atttactgtc tacatgactg catggatgtt acactgatct tcttctgccc ttggactggg 1260
acttatactt ggtccccctg attctcaggc cttcagagtt ggatcagaac ttacaacatc 1320
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catttcacca cacacacacaca cacacacaca cacacatata ccatttgcc 1500
tgtttctctg aagaactctg acaaaaataca gatTTTgttgc ctgaaaagaga ttctagagga 1560
acggaattttt aaggataaat tttctgaattt ggttatgggg ttcttgcattt tggctctata 1620
atctaatttag atataaaattt ctggtaactt tatttacaat aataaagata gcaactatgtg 1680

ttcaaa CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
1686

<210> 148

<211> 347

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15

Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30

Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45

Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60

Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80

Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Val Tyr
100 105 110

Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115 120 125

Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130 135 140

Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145 150 155 160

Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
165 170 175

Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180 185 190

Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205

Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210 215 220

Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225 230 235 240

Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255

Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260 265 270

Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285

Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly

290 295 300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320
 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335
 His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 149
ttcagctcat cacttcacc tgcc 24

<210> 150
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 150
ggctcataca aaataccact aggg 24

<210> 151
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 151 gggccttccac cgctgtgaag ggcgggtgga ggtggAACAG aaaggccagt 50

<210> 152
<211> 1427
<212> DNA
<213> *Homo sapiens*

<400> 152	actgcactcg	gttctatcga	ttgaattccc	cggggatcct	ctagagatcc	ctcgacctcg	60
acccacgcgt	ccgcggacgc	gtggggcgac	gcgtgggccc	gctaccagga	agagtctgcc	120	
gaagggtgaag	gccatggact	tcatcacctc	cacagccatc	ctgcccctgc	tgttcggtg	180	
cctgggcgtc	ttcggcctct	tccggctgct	gcagtggggt	cgcggaaagg	cctacctgcg	240	
gaatgcgtg	gtgggtatca	caggcgccac	ctcagggctg	ggcaaagaat	gtgcaaagaat	300	
cttctatgct	gccccgtcta	aactgggtct	ctgtggcccg	aatggtgggg	ccctagaaaga	360	
gctcatcaga	gaacttaccg	cttctcatgc	caccaaggt	cagacacaca	agccttactt	420	
ggtgcacctc	gacctcacag	actctggggc	catagttgca	gcagcagctg	agatctgcg	480	
gtgcttggc	tatgtcgaca	tacttgtcaa	caatgctgg	atcagctacc	gtggtaccat	540	
catggacacc	acagtggatq	tggacaqaq	qqtcatggq	acaactact	ttqgccccq	600	

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
 catcagcagc atccagggca agatgagcat tcctttcga tcagcatatg cagcctccaa 720
 gcaccaacc caggcttct ttgactgtct gcgtgccgag atgaaacagt atgaaattga 780
 ggtgaccgtc atcagccccg gctacatcca caccacccctc tctgtaaatg ccatcaccgc 840
 ggtatggatct aggtatggag ttatggacac caccacagcc cagggccgaa gcccgttgg 900
 ggtggcccgat gatgttcttg ctgctgtggg gaagaagaag aaagatgtga tcctggctga 960
 cttaactgcct tccttggctg tttatcttcg aactctggct cctgggctct tcttcagcct 1020
 catggccctc agggccagaa aagagcggaa atccaagaac tccttagtact ctgaccagcc 1080
 agggccaggc cagagaagca gcactcttag gcttgcttac tctacaagggg acagttgcat 1140
 ttgtttagac ttaatggag atttgtctca caagtggaa agactgaaga aacacatctc 1200
 gtgcagatct gctggcagag gacaatcaa aacgacaaca agcttcttc cagggtgagg 1260
 gaaaaactt aaggaataaa tatggagctg gggtaaca ctaaaaacta gaaataaaca 1320
 tctcaaacag taaaaaaaaaa aaaaaaggc ggccgcgact cttagagtca cctgcagaag 1380
 cttggccgccc atggcccaac ttgttattt cagcttataa tggttac 1427

<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

Met	Asp	Phe	Ile	Thr	Ser	Thr	Ala	Ile	Leu	Pro	Leu	Leu	Phe	Gly	Cys
1								5			10			15	

Leu	Gly	Val	Phe	Gly	Leu	Phe	Arg	Leu	Leu	Gln	Trp	Val	Arg	Gly	Lys
								20	25				30		

Ala	Tyr	Leu	Arg	Asn	Ala	Val	Val	Val	Ile	Thr	Gly	Ala	Thr	Ser	Gly
							35	40			45				

Leu	Gly	Lys	Glu	Cys	Ala	Lys	Val	Phe	Tyr	Ala	Ala	Gly	Ala	Lys	Leu
							50	55			60				

Val	Leu	Cys	Gly	Arg	Asn	Gly	Gly	Ala	Leu	Glu	Glu	Leu	Ile	Arg	Glu
65							70			75			80		

Leu	Thr	Ala	Ser	His	Ala	Thr	Lys	Val	Gln	Thr	His	Lys	Pro	Tyr	Leu
							85		90			95			

Val	Thr	Phe	Asp	Leu	Thr	Asp	Ser	Gly	Ala	Ile	Val	Ala	Ala	Ala	
100							105				110				

Glu	Ile	Leu	Gln	Cys	Phe	Gly	Tyr	Val	Asp	Ile	Leu	Val	Asn	Asn	Ala
							115	120			125				

Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Ile	Met	Asp	Thr	Thr	Val	Asp	Val	Asp
130							135			140					

Lys	Arg	Val	Met	Glu	Thr	Asn	Tyr	Phe	Gly	Pro	Val	Ala	Leu	Thr	Lys
145				150				155				160			

Ala	Leu	Leu	Pro	Ser	Met	Ile	Lys	Arg	Arg	Gln	Gly	His	Ile	Val	Ala
								165	170			175			

Ile	Ser	Ser	Ile	Gln	Gly	Lys	Met	Ser	Ile	Pro	Phe	Arg	Ser	Ala	Tyr
							180	185			190				

Ala	Ala	Ser	Lys	His	Ala	Thr	Gln	Ala	Phe	Phe	Asp	Cys	Leu	Arg	Ala
							195	200			205				

Glu	Met	Glu	Gln	Tyr	Glu	Ile	Glu	Val	Thr	Val	Ile	Ser	Pro	Gly	Tyr
210						215				220					

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
290 295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156

tcatactgtt ccatctcgac acgc

24

<210> 157

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 157 aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158

<211> 1771

<212> DNA

<213> Homo sapiens

<400> 158

cccacgcgtc cgctgggttt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
 aaaaaaaaaa acacaccaaa cgctcgcagc cacaaaaggg atgaaaatttc ttctggacat 120
 ctcctgctt ctcccgttac tgatcgctg ctccttagag tccctcgta agcttttat 180
 tcctaagagg agaaaatcag tcaccggcga aatcgctgtg attacaggag ctgggcattgg 240
 aattggaga ctgactgctt atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
 tataaataag catggactgg aggaaacagc tgccaaatgc aaggactgg gtgccaaggt 360
 tcatacctt gtggtagact gcagcaaccg agaagatatt tacagctctg caaagaaggt 420
 gaaggcagaa attggagatg ttatgtatTTT agtaaataat gctgggtgtag tctatacatc 480
 agattgttt gctacacaag atcctcagat tgaaaagact tttgaagttt atgtacttgc 540
 acatttctgg actacaaaagg catttcttcc tgcaatgacg aagaataacc atggccatat 600
 tgtcactgtg gcttcggcag ctggacatgt ctcggtcccc ttcttactgg cttactgttc 660
 aagcaagttt gctgctgtt gatttcataa aactttgaca gatgaactgg ctgccttaca 720
 aataactgga gtcaaaacaa catgtctgtg tcctaatttc gtaaacactg gcttcataa 780
 aaatccaagt acaagtttg gaccactct ggaacctgag gaagtggtaa acaggctgat 840
 gcatgggatt ctgactgac agaagatgt ttttatttca tcttctatag ctttttaac 900
 aacatggaa aggatccttc ctgagcgttt cctggcagtt ttaaaacgaa aaatcagtgt 960
 taagtttgc gcatgtttagt gatataaaat gaaagcgc当地 taagcacca gttttctgaa 1020
 aactgatata ccagggttagt gttgatgtca tctaataatgt ccagaattttt aatgtttgaa 1080
 cttctgtttt ttcttaattat ccccttttca tcaatatcat tttttaggtt ttggcagtct 1140
 tcatttacta ccacttgc tttagccaaa agctgattac atatgatata aacagagaaa 1200
 tacttttaga ggtgacttta aggaaaatga agaaaaagaa cccaaatgac tttttaaaaa 1260
 taatttccaa gattattttt ggctcacctg aaggcttgc aaaatttgc ccataaccgt 1320
 ttatttaaca tatattttt ttttgattt cacttaaattt ttgtataattt tttttttttt 1380
 tttctgttctt acataaaaatc agaaacttca agctctctaa ataaaatgaa ggactatatc 1440
 tagtggattt tcacaatgaa tatcatgaa tctcaatggg tagtttcat cttaccatt 1500
 gccactctgt ttcctgagag atacccatca ttccaaatgcc aaacatttct gcacaggaa 1560
 gctagaggtg gatacacgtg ttgcaagttt aaaagcatca ctgggattt aggagaattg 1620
 agagaatgta cccacaaaatg gcagcaataa taaatggatc acacttaaaa aaaaaaaaaaa 1680
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1740
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1771

<210> 159

<211> 300

<212> PRT

<213> Homo sapiens

<400> 159

Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Pro Leu Leu Ile Val
 1 5 10 15

Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
 20 25 30

Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
 35 40 45

Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
 50 55 60

Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
 85 90 95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 160

ggtaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 161

atccccatgca tcagcctgtt tacc

24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 162

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 162

gctggtag tctatacatc agattgttt gctacacaag atccttag

48

<210> 163

<211> 2076

<212> DNA

<213> Homo sapiens

<400> 163

ccacgcgtc cgcggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgccgc 60
tcaggagga gcaccgactg cgccgcaccc tgagagatgg ttgggtccat gtggaaagggtg 120
attgttgcg tggtcctgtt gatgcctggc ccctgtatg ggctgtttcg ctccctatac 180
agaagtgtt ccatgccacc taaggagac tcaggacacg cattatttct cacccttac 240
attgaagctg ggaagatcca aaaaggaaga gaatttgatg tggtcggccc tttccagga 300
ctgaacatga agagttatgc cggcttcctc accgtgaata agacttacaa cagcaacctc 360
ttcttcgtt tttcccaagc tcagatacag ccagaagatg ccccaagtgt tctctggcta 420
cagggtggc cgggagggtc atccatgtt ggactcttg tggaaatcg gccttatgtt 480
gtcacaagta acatgaccc tgcgtacaga gacttccct ggaccacaac gctctccatg 540
ctttacattg acaatccagt gggcacaggc ttcaatgtt ctgtatgatac ccacggatat 600
gcagtcata gaggacgtat agcacggat ttatacagtg cactaattca gttttccag 660
atattcctg aatataaaaa taatgacttt tatgtcactg gggagtctt tgcaggaaaa 720
tatgtgccag ccattgcaca cctcatccat tccctcaacc ctgtgagaga ggtgaagatc 780
aacctgaacg gaatttgctat tggagatgga tattctgtatc ccgaatcaat tataggggc 840
tatgcagaat tcctgtacca aattggctt tggatgaga agcaaaaaaa gtacttccag 900
aagcatgtcc atgaatgcata agaacacatc aggaagcaga actgggttga ggcctttaga 960
atactggata aactactaga tggcactta acaagtgtatc cttcttactt ccagaatgtt 1020
acaggatgta gtaattacta taacttttg cggtgacgg aacctgagga tcagcttac 1080
tatgtgaaat ttttgtact cccagaggtg agacaagcca tccacgtgg gaatcagact 1140
ttaatgtatg gaactatagt tggaaatgtac ttgcgagaag atacagtaca gtcagtaag 1200
ccatgtaa ctgaaatcat gaataattat aagggtctga tctacaatgg ccaactggac 1260
atcatctgtgg cagctgcct gacagagcgc tccttgcgtt gcatggactg gaaaggatcc 1320
caggaataca agaaggcaga aaaaaaagt tggaaatgtt ttaaatctga cagtgaagtg 1380
gctggttaca tccggcaagc gggtgactt catcaggtaa ttatcgagg tggaggacat 1440
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cattgctgaa aaaaaaatcg taaaacaga aaatgtcata ggaataaaaaa aattatcttt 1620
tcatatctgc aagattttt tcatcaataa aaattatctt tggaaacaagt gagctttgt 1680
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taacaaacaa agctgtacca tcttttctg ccaataacag aagttggca tgccgtgaag 1920
gtgttggaa atattattgg ataagaatag ctcattatc ccaataaaat ggatgaagct 1980
ataatagttt tggggaaaag attctcaat gtataaagtc ttagaacaaa agaattcttt 2040
gaaataaaaaa tattatataat aaaagtaaaaa aaaaaa 2076

<210> 164

<211> 476

<212> PRT

<213> Homo sapiens

<400> 164

Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met

1

5

10

15

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30

Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45

Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60

Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
65 70 75 80

Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
85 90 95

Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
100 105 110

Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
115 120 125

Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
130 135 140

Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
145 150 155 160

Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
165 170 175

Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
180 185 190

Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
195 200 205

Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
210 215 220

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225 230 235 240

Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
340 345 350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
435 440 445

Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
450 455 460

Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 165

ttccatgcc a cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 167

agctctcaga ggctggcat aggg

24

<210> 168

<211> 50

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

cgaggcgttt tccggctccg gaatggcaca tgtggaaatc ccagtcttgt tggctacaac 60
 attttccct ttcctaacaat gttctaacat ctgttctaac agctatgtat caggggttct 120
 tcttgcgttga gaagaaaggc ctgagggcag acgcggcac tctcaactcg ggtgaccagc 180
 tccttcctc tctgtggata acagagcatg agaaatgtaa gagatgcagc ggagtggatg 240
 gatggaaatgc taaaatagga aggaattttgc tttgtcaatat cagactctgg gacgatgtga 300
 cctggagagc ctgggggagg gcctgcctaa caagcttca aaaaacagga gcgacttcca 360
 ctgggtctggg ataagacgtg ccggtaggat agggaaagact gggtttagtc ctaatatcaa 420
 attgactggc tgggtgaact tcaacagccct ttttacccctt ctggggagatg aaaacatgg 480
 cttaaaggc cagaaataga gatgtttgt aaaaataaaat tttaaaaaaa gcaagtattt 540
 tatagataa aggctagaga ccaaaataga taacaggat ccctgaacat tcctaaaggagg 600
 gagaatgtttaaaaata gaaaaacacaa aatgcagaag gaggagactc acagactaa 660
 accagatgg ggacccttggg tcaggccagc ctcttgcctt cttccggaaa ttatttttgg 720
 tctgaccact ctgccttgc ttttgcagaa tcatgtgagg gccaaccggg gaaggtggag 780
 cagatgagca cacacaggag ccgtctccctt accggccccc ctctcagcat ggaacagagg 840
 cagccctggc cccggccctt ggaggtggac agccgtctg tggctctgtc ctcagtggc 900
 tgggtgtgc tggccccc accgtgcacc gtccaccaag ggacgggggc cgtctatgt 1020
 aatcgtgact ggaccttcaa ccacttgacc gtccaccaag ggacgggggc ggctcataag 1080
 ggggcatca accgggtcta taagtcgaca ggcaacctga ccatccaggt ctctgagaac 1140
 acagggccag aagaggacaa caagtctcgat taccggcccc tcatcgatgc 1200
 gaagtgtca ccctcaccaa caatgtcaac aagctgtca tcattgacta ctcgtgc 1260
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 cgagaccctg agtcctcagc catgtcgac tatgagctac acagcgattt tgcctccct 1560
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 cagtttaccc accccggccga tgactctgcc ctgtgtgcct tccctatccg ggccatcaac 1980
 ttgcagatca aggagcgctt gcagtcctgc taccaggggc agggcaacct ggagctcaac 2040
 tggctgtgg ggaaggacgt ccagtgcacg aaggcgccctg tcccccattcgat tgataacttc 2100
 tgtggactgg acatcaacca gcccctggaa ggctcaactc cagttggaggg cctgaccctg 2160
 tacaccacca gcagggaccc catgacccctt gtggctccctt acgtttacaa cggctacagc 2220
 gtggtttttgg tggggactaa gagttggcaag ctggaaaaagg taagagtcta tgagttcaga 2280
 tgctccaatgc catttcaccc cctcagcaaa gagtccctt tggaaaggtag ctattgggtgg 2340
 agatttaact ataggcaact ttatttctt ggggaacaaaaa ggtgaaatgg ggaggttaaga 2400
 aggggttaat ttgtgtactt agcttcttagc tacttcctcc agccatcagt cattgggtat 2460
 gtaagaatgc caagcgattt tcaatatttc ccaaacttta agaaaaaact ttaagaaggt 2477
 acatctgcaaa aagcaaa

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 170
Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
1 5 10 15
Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
20 25 30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
35 40 45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
50 55 60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
65 70 75 80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
85 90 95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
100 105 110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
115 120 125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
130 135 140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
145 150 155 160
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
165 170 175
Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
180 185 190
Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
195 200 205
Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
210 215 220
Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
225 230 235 240
Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
245 250 255
Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
260 265 270
Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
275 280 285
Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
290 295 300
Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
305 310 315 320
Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
340 345 350
Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
355 360 365
Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
370 375 380
Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
385 390 395 400
His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
405 410 415
Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
420 425 430
Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
435 440 445
Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171
tggaataccg cctcctgcag 20

<210> 172
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc

24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
ggactcactg gcccaggcct tcaatatcac cagccaggac gat

43

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)..(1683)
<223> a, t, c or g

<400> 174
aggctccgc gcgccgctga gtgcggactg gagtggaaac cgggtcccc ggccttagag 60
aacacgcgt gaccacgtgg agcctccggc ggaggccggc cgcacgctg ggactccgtc 120
tgctggctgt cttgggcttc ctgggtctcc gcaggctgga ctggagcacc ctggccctc 180
tgcggctccg ccatcgacag ctggggctgc aggccaaggg ctggacttc atgctggagg 240
attccacattt ctggatcttc ggggctcca tccactattt ccgtgtgccc agggagtaact 300
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360
cgtggaaacct gcatgagcca gaaagaggca aatttgactt ctctggaaac ctggacctgg 420
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgcgt ccaggcccc 480
acatctgcag tgagatggac ctcggggct tgcccagctg gctactccaa gaccctggca 540
tgaggcttag gacaacttac aagggcttca ccgaagcagt ggacctttat ttgaccacc 600
ttagtccag ggtggtgcca ctccagttaca agcgtggggg acctatcatt gccgtgcagg 660
tggagaatga atatggttcc tataataaaag accccgcata catgccctac gtcaagaagg 720
caactggagga ccgtggcatt gtggaaactgc tcctgacttc agacaacaag gatgggtgt 780
gcaaggggat tgcagggttgc gtctggcca ccatcaactt gcagtcaaca cacgagctgc 840
agactactgac cacccttc ttcacgtcc aggggactca gccaagatg gtgatggagt 900
actggacggg gtgggttgac tcgtggggag gcccctcacaa tatctggat tcttctgagg 960
ttttggaaac cgtgtctgcc attgtggacg ccggctctc catcaaccc tacatgttcc 1020
acggaggcac caactttggc ttcatgaatg gagccatgca cttccatgac tacaagtca 1080
atgtcaccag ctatgactat gatgtgtgc tgacagaagc cggcgattac acggccaagt 1140
acatgaagct tcgagacttc ttccgctcca tctcaggcat ccctctccct cccccacctg 1200
accctttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260
acgcctcaa gtacctgggg gagccaatca agtctgaaaa gcccattcaac atggagaacc 1320
tgccagtc当地 tggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380
cctcgctgg catcctcagt ggccacgtgc atgatcgaaa gcagggtgtt gtgaacacag 1440
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500
acaccgtct gaggatctg gtggagaatc gtggggcgagt caactatggg gagaatattg 1560
atgaccacgc caaaggctta attggaaatc tctatctgaa tgattcaccc ctgaaaaact 1620
tcagaatcta tagcctggat atgaagaaga gcttcttca gaggttcggc ctggacaaat 1680
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggttagc ttgtccatca 1740
gctccacgc ttgtgacacc ttctgaaac tggagggctg ggagaagggg ttgttattca 1800
tcaatggcca gaaccttggc cgttactgga acattggacc ccagaagacg ctttaccc 1860
caggtccctg gttgagcagc ggaatcaacc aggtcatgt ttttggaggacgatggcgg 1920
gccctgcatt acagttcactg gaaaccccccc acctggcag gaaaccgtac attaagttag 1980
cggtggcacc ccctccctgt ggtggccagtggagactgccc gccctctt gacctgaagc 2040

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ctggtggtcg ctgccccacc cctcaactgca aaagcatctc cttaaatgtgc aacctcagg 2100
 actgggggct acagtctgcc cctgtctcag ctcaaaaaccc taagcctgca gggaaagg 2160
 ggtatggctct gggcctggct ttgttgcata tggctttcct acagccctgc tcttgcctc 2220
 aggctgtcgg gctgtctcta ggggtgggagc agctaattcag atcggccagc ctttggccct 2280
 cagaaaaagt gctgaaacgt gcccctgcac cggacgtcac agccctgcga gcatctgtc 2340
 gactcaggcg tgctcttgc tggttccctgg gaggcttggc cacatccctc atggcccat 2400
 tttatccccg aataatcctggg tttgttgcata gtgttagaggg tggggaaagg 2460
 tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaaggaa 2520
 ctcggcgtga gaaacatgtg actttccctt tcccttccca ctcgtgtc 2580
 gacagctgg gctggagaaa cagaatcctt caccctgcgt cttcccaagt tagcagg 2640
 ctctgggtt cagtggggg gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
 catccaggaa ggaggacaga aggcccagct cacatgtgag tcctggcaga agccatggcc 2760
 catgtctgca catccaggaa ggaggacaga aggcccagct cacatgtgag tcctggcaga 2820
 agccatggcc catgtctgca catccaggaa ggaggacaga aggcccagct cacatgtgag 2880
 tcctggcaga agccatggcc catgtctgca catccaggaa ggaggacaga aggcccagct 2940
 cagtggcccc cgctcccccac ccccacgccc cgaacagcag gggcagagca gccctccctc 3000
 gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggctt 3060
 ggctcaactgt cctgagttgc agtaaagcta taaccttgaa tcacaa 3106

<210> 175

<211> 636

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (539)

<223> Any amino acid

<400> 175

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1 5 10 15

Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
 20 25 30

Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
 50 55 60

Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80

Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95

Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110

Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
 115 120 125

Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
 130 135 140

Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160

Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
 515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
 530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
 545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
 565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
 580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
 595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
 610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
 625 630 635

<210> 176

<211> 2505

<212> DNA

<213> Homo sapiens

<400> 176

ggggacgcgg	agctgagagg	ctccgggcta	gctaggtgta	ggggtggacg	ggtcccagga	60
ccctggtag	ggttctctac	ttggccttcg	gtgggggtca	agacgcaggc	acctacgcca	120
aaggggagca	aagccgggct	cggcccgagg	ccccccaggac	ctccatctcc	caatgttgg	180
ggaatccgac	acgtgacggt	ctgtccgccc	tctcagacta	gaggagcgct	gtaaacgcca	240
tggctcccaa	gaagctgtcc	tgccttcgtt	ccctgctgct	gccgctcagc	ctgacgctac	300
tgctgccccca	ggcagacact	cggtcgttcg	tagtgatag	gggtcatgac	cggtttctcc	360
tagacggggc	cccgttccgc	tatgtgtctg	gcagcctgca	ctactttcgg	gtaccgcggg	420
tgcttgggc	cgaccggctt	ttgaagatgc	gatggagcgg	cctcaacgccc	atacagttt	480
atgtgccctg	gaactaccac	gagccacagc	ctggggctca	taactttaat	ggcagccggg	540
acctcattgc	ctttctgaat	gaggcagctc	tagcgaacct	gttggtcata	ctgagaccag	600
gaccttacat	ctgtgcagag	tgggagatgg	ggggctctcc	atccctgggt	cttcgaaaac	660
ctgaaattca	tctaagaacc	tcagatccag	acttcttgc	cgcagtggac	tcctggttca	720
aggcttgc	gcccggccat	tatccatggc	tttacatggc	tggggcaac	atcattagca	780
ttcagggtga	gaatgaatat	ggtagctaca	gagcctgtga	cttcagctac	atgaggcact	840
tggctgggct	cttccgtgca	ctgcttaggag	aaaagatctt	gcttttcacc	acagatgggc	900
ctgaaggact	caagtgtggc	tccctccggg	gactctatac	cactgttagat	tttggcccaag	960
ctgacaacat	gacaaaatc	tttaccctgc	ttcggaaagta	tgaaccccat	gggccatgg	1020
taaactctga	gtactacaca	ggctggctgg	attactgggg	ccagaatcac	tccacacgg	1080
ctgtgtcagc	tgttaaaaaa	ggactagaga	acatgctcaa	gttgggagcc	agtgtgaaca	1140
tgtacatgtt	ccatggaggt	accaactttt	gatattggaa	tggtggccgt	aagaagggac	1200
gcttccttcc	gattactacc	agctatgact	atgatgcacc	tatactgaa	gcaggggacc	1260
ccacacctaa	gcttttgc	tttcggatg	tcatcagcaa	gttccaggaa	gttccttgg	1320
gaccttacc	tcccccgagc	cccaagatga	tgcttggacc	tgtgactctg	cacctgggt	1380
ggcatttact	ggctttccta	gacttgcttt	gccccctgtgg	gcccattcat	tcaatcttgc	1440
caatgacctt	tgaggctgtc	aaggcaggacc	atggcttcat	gttgtaccga	acctataatga	1500
cccataccat	ttttgagcca	acaccattct	gggtgccaaa	taatggagtc	catgaccgt	1560
cctatgtat	ggggatggg	gtgttccagg	gtgttgtgaa	gcgaaatatgt	agagacaaac	1620
tatttttgac	ggggaaaactg	gggtccaaac	tggatatctt	ggtgagaaac	atggggaggc	1680
tcagcttgg	gtctaacagc	agtgacttca	agggcctgtt	gaagccacca	attctgggc	1740
aaacaatcct	tacccagtgg	atgatgttcc	ctctgaaaat	tgataacctt	gtgaagtgg	1800
ggttccct	ccagttgcca	aaatggccat	atcctcaagc	tccttctggc	cccacattct	1860
actccaaaac	atttccaatt	ttaggctcag	ttggggacac	atttctatat	ctacctggat	1920
ggaccaaggg	ccaagtctgg	atcaatgggt	ttaacttggg	ccggtactgg	acaaagcagg	1980

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ggccacaaca gaccctctac gtgccaagat tcctgctgtt tcctagggga gccctcaaca 2040
 aaattacatt gctggaacta gaagatgtac ctctccagcc ccaagtccaa tttttggata 2100
 agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
 atacactgag tgcctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
 ggtggctcat gcctgttaatc ccagcactt gggaggctga gacgggtgga ttacctgagg 2280
 tcaggacttc aagaccagcc tggccaaatc ggtgaaaccc cgttccact aaaaatacaa 2340
 aaattagccg ggcgtatgg tggcaccc tcatacccagc tacttgggag gctgagggca 2400
 ggagaattgc ttgaatccag gaggcagagg ttgcagttag tggagggtgtt accactgcac 2460
 tccagcctgg ctgacagtga gacactccat ctaaaaaaaaaaaa 2505

<210> 177

<211> 654

<212> PRT

<213> Homo sapiens

<400> 177

Met	Ala	Pro	Lys	Lys	Leu	Ser	Cys	Leu	Arg	Ser	Leu	Leu	Leu	Pro	Leu
1					5			10					15		

Ser	Leu	Thr	Leu	Leu	Leu	Pro	Gln	Ala	Asp	Thr	Arg	Ser	Phe	Val	Val
					20			25					30		

Asp	Arg	Gly	His	Asp	Arg	Phe	Leu	Leu	Asp	Gly	Ala	Pro	Phe	Arg	Tyr
						35		40				45			

Val	Ser	Gly	Ser	Leu	His	Tyr	Phe	Arg	Val	Pro	Arg	Val	Leu	Trp	Ala
					50		55				60				

Asp	Arg	Leu	Leu	Lys	Met	Arg	Trp	Ser	Gly	Leu	Asn	Ala	Ile	Gln	Phe
					65		70			75			80		

Tyr	Val	Pro	Trp	Asn	Tyr	His	Glu	Pro	Gln	Pro	Gly	Val	Tyr	Asn	Phe
					85		90				95				

Asn	Gly	Ser	Arg	Asp	Leu	Ile	Ala	Phe	Leu	Asn	Glu	Ala	Ala	Leu	Ala
					100		105				110				

Asn	Leu	Leu	Val	Ile	Leu	Arg	Pro	Gly	Pro	Tyr	Ile	Cys	Ala	Glu	Trp
					115		120				125				

Glu	Met	Gly	Gly	Leu	Pro	Ser	Trp	Leu	Leu	Arg	Lys	Pro	Glu	Ile	His
					130		135			140					

Leu	Arg	Thr	Ser	Asp	Pro	Asp	Phe	Leu	Ala	Ala	Val	Asp	Ser	Trp	Phe
					145		150			155			160		

Lys	Val	Leu	Leu	Pro	Lys	Ile	Tyr	Pro	Trp	Leu	Tyr	His	Asn	Gly	Gly
					165		170			175					

Asn	Ile	Ile	Ser	Ile	Gln	Val	Glu	Asn	Glu	Tyr	Gly	Ser	Tyr	Arg	Ala
					180		185			190					

Cys	Asp	Phe	Ser	Tyr	Met	Arg	His	Leu	Ala	Gly	Leu	Phe	Arg	Ala	Leu
					195		200			205					

Leu	Gly	Glu	Lys	Ile	Leu	Leu	Phe	Thr	Thr	Asp	Gly	Pro	Glu	Gly	Leu
					210		215			220					

Lys	Cys	Gly	Ser	Leu	Arg	Gly	Leu	Tyr	Thr	Thr	Val	Asp	Phe	Gly	Pro
					225		230			235			240		

Ala	Asp	Asn	Met	Thr	Lys	Ile	Phe	Thr	Leu	Leu	Arg	Lys	Tyr	Glu	Pro
					245		250			255					

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile
340 345 350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Pro Ser Pro
355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu
370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu
385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr
405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val
420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val
435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 179

tggaccaaattc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 181

ccagctatga ctatgtatgc cc

22

<210> 182

<211> 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182

tggcacccag aatggtgtt gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

gcttgaaca	cgtctgcaag	cccaaagtt	agcatctgat	tggttatgag	gtatggagt	60
gcacccacaa	tatggcttac	atgtgaaaaa	agcttctcat	cagttacata	tccattattt	120
gtgttatgg	ctttatctgc	ctctacactc	tcttctgggt	attcaggata	cctttgaagg	180
aatattctt	cgaaaaaagtc	agagaagaga	gcagtttag	tgacattcca	gtatgtcaaaa	240
acgattttgc	gttccttctt	cacatggtag	accagtatga	ccagctata	tccaagcggt	300
ttggtgtgtt	cttgcagaa	gttagtggaa	ataaaacttag	ggaatttagt	ttgaaccatg	360
agtggacatt	tgaaaaaactc	aggcagcaca	tttcacgca	cgtttcaggac	aagcaggagt	420
tgcacatgtt	catgctgtcg	gggggtcccc	atgctgtctt	tgacactaca	gacctggatg	480
tgctaaagct	tgaactaatt	ccagaagcta	aaattccgtc	taagatttct	caaatgacta	540
acctccaaga	gctccaccc	tgccactgccc	ctgcaaaagt	tgaacagact	gttttttagct	600
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cctgggtgt	tttgctcaaa	aacccctcgag	agttgtactt	aataggcaat	ttgaactctg	720
aaaacaataa	gatgatagga	cttgaatctc	tccgagagtt	gcggcacctt	aagatttcc	780
acgtgaagag	caatttgacc	aaagttccct	ccaaacatc	agatgtggct	ccacatctta	840
caaaggtagt	cattcataat	gacggcacta	aactcttgg	actgaacagc	cttaagaaaa	900
tgtatgaatgt	cgctgagctg	gaactccaga	actgtgagct	agagagaatc	ccacatgcta	960
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agggaaaggaa	aaattataat	cactaatctt	ggttctttt	aaattgttt	taacttggat	1860
gctgccgcta	ctgaatgtt	acaaatttgc	tgcctgctaa	agtaaatgat	taaattgaca	1920
ttttcttact	aaaaaaaaaa	aaaaaaa				1947

<210> 185

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 501
<212> PRT
<213> Homo sapiens

<400> 185

Met Ala Tyr Met Leu Lys Lys Leu Leu Ile Ser Tyr Ile Ser Ile Ile
1 5 10 15

Cys Val Tyr Gly Phe Ile Cys Leu Tyr Thr Leu Phe Trp Leu Phe Arg
20 25 30

Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
35 40 45

Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
50 55 60

Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
65 70 75 80

Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
85 90 95

Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
100 105 110

Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
115 120 125

Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
145 150 155 160

Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
180 185 190

Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
195 200 205

Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
210 215 220

Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
225 230 235 240

Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
245 250 255

Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
275 280 285

Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
290 295 300

Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305	310	315	320
Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn			
325	330	335	
Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu			
340	345	350	
Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val			
355	360	365	
Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile			
370	375	380	
Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu			
385	390	395	400
His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys			
405	410	415	
Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser			
420	425	430	
Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu			
435	440	445	
Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg			
450	455	460	
Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr			
465	470	475	480
Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro			
485	490	495	
Phe Ala Asn Gly Ile			
500			

<210> 186

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 186

cctccctcta ttacccatgt c

21

<210> 187

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 187

gaccaacttt ctctgggagt gagg

24

<210> 188

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acagactcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

cccacgcgtc	cgcccttctc	tctggacttt	gcatttccat	tcctttcat	tgacaaactg	60
actttttta	tttctttttt	tccatctctg	ggccagctt	ggatcctagg	ccgcccctggg	120
aagacattt	tgttttcacac	acataaggat	ctgtgttgg	ggtttcttct	tcctcccttg	180
acattggcat	tgcttagtgg	ttgtgtgggg	agggagacca	cgtgggctca	gtgcttgctt	240
gcacttatct	gccttaggtac	atcgaagtct	tttgacctcc	atacagtgtat	tatgcctgtc	300
atcgctgggt	gtatcctggc	ggcccttgc	ctgctgatag	ttgtcgtgt	ctgtctttac	360
ttcaaaaat	acaacgcgc	aaaagctgca	aaggaacctg	aagctgtggc	tgtaaaaaat	420
cacaacccag	acaagggtgt	gtgggccaag	aacagccagg	ccaaaacat	tgccacggag	480
tcttgctct	ccctgcag	ctgtgaagg	tatagaatgt	gtggcagttt	tgattccctg	540
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gcagagccct	gaagacttca	atgatgtca	tgaggccacc	tggttgtgat	gtgcaggcac	660
agaagaaagg	cacagctccc	catcagttc	atggaaaata	actcagtgtcc	tgctggaaac	720
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aatatggcag	agacccacaa	agccatgatc	ctgcaactca	atcccagtga	gaactgcacc	1140
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tccagtagat	tgacgtttca	aatagttact	gactcagca	gaattcaaag	aactgtcttt	1380
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gtcccttta	atggatgtgg	tacaatcaga	aaggtagaa	atcagtcaat	tacttacacc	1980
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gaaactccaa	accagcctt	caacagtgt	catctt	ccttcatgt	tctagctctg	2700
aatgttgtga	ctgtagcgac	aatcacagt	aggcattt	taaatcaacg	ggcagactac	2760

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

aaataccaga agctgcagaa ctattaacta acaggtccaa ccctaagtga gacatgttc 2820
 tccagatgc caaaggaaat gctacctcggt ggcacacat attatgaata aatgaggaag 2880
 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190

<211> 607

<212> PRT

<213> Homo sapiens

<400> 190

Met Glu Leu Val Arg Arg Leu Met Pro Leu Thr Leu Leu Ile Leu Ser
 1 5 10 15

Cys Leu Ala Glu Leu Thr Met Ala Glu Ala Glu Gly Asn Ala Ser Cys
 20 25 30

Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45

Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60

Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80

Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95

Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125

Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140

Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160

Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175

Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190

Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205

Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220

Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240

Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255

Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270

Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
595 600 605

<210> 191
<211> 21

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g

21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 192

tttgatgacg attcgaaggt gg

22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

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ctgctgctgc	cggccgcggcc	gtgcctgtcc	cacagcggca	cgcgcttcga	ccccacccctgg	180
gagtccctgg	acgccccgcca	gctggcccg	tggtttgacc	aggccaaagg	cggcatcttc	240
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caaaaaggaaa	agataccgaa	gtatgtggaa	tttatgaaag	ataattaccc	tcctagtttc	360
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cccacactag	atggcaccat	ttctgttagtt	tttgaggagc	gactgaggca	agtgggggtcc	1140
tggctaaaag	tcaatggaga	agcttattat	gaaacactt	cctggcgatc	ccagaatgac	1200
actgtcaccc	cagatgtgt	gtacacatcc	aagcctaaag	aaaaattagt	ctatgccatt	1260
tttcttaaat	ggcccacatc	aggacagctg	ttcccttgcc	atcccaaagc	tattctgggg	1320
gcaacagagg	tgaaactact	gggccatgga	cagccaccta	actggattc	tttggagcaa	1380

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 ttaaatttacc catgtAACCA ttttaactct ccagtgcact ttgccattaa agtctttca 1680
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 taggacatta tggaaacactg ccagacgtta taaaactgt atgcttaggc tacactacat 2220
 ttataaaaaaa aagttttctt ttctcaatt ataaattaac ataaatgtac tggtaacttta 2280
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 taaactcatt gtgcaaatgt aa 2362

<210> 195

<211> 467

<212> PRT

<213> Homo sapiens

<400> 195

Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
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Leu Leu Leu Leu Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30

Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45

Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
 50 55 60

Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
 65 70 75 80

Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
 85 90 95

Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
 100 105 110

Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
 115 120 125

Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
 130 135 140

Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
 145 150 155 160

Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
 165 170 175

Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
 180 185 190

Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
 195 200 205

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
 210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
 225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
 245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
 260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
 275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
 290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
 305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
 325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gln Pro Leu Asn
 420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460

Asn Val Ile
 465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 196

tggtttgacc aggccaaagt tgg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 198

aacttgcagc atcagccact ctgc

24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 199

ttccgtgccc agcttcggta gcgagtggtt ctgggtggat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

agcagggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
gttccagaac ttcctatccg gactagttt tgagcatctg cctctcatat caccagtggc 120
catctgaggt gtttccctgg ctctgaaggg gttaggcacga tggccagggtg cttcagcctg 180
gtgttgcttc tcacccatccat ctggaccacg aggctctgg tccaaggctc tttgcgtgca 240
gaagagcttt ccatcccggt gtcatcgaga attatggggta tcacccctgt gaggaaaaag 300
gcgaaccagc agctgaattt cacagaagct aaggaggccct gttagctgtc gggactaagt 360
ttggccggca aggaccaagt tgaaacagcc ttgaaagctt gcttgaaac ttgcagctat 420
ggctgggttg gagatggatt cgtggtcatc tctaggattt gccccaaaccc caagtgtggg 480
aaaaatgggg tgggtgtcctt gatttggaaag gttccagtgta gcccacagtt tgccgttat 540
tgttacaact catctgatac ttggactaac tcgtgcattc cagaaattat caccacccaaa 600
gatcccatat tcaacactca aactgcaaca caaacaacag aatttattgt cagtgcacagt 660
acctactcgg tggcatcccc ttactctaca atacctgccc ctactactac tcctcctgt 720
ccagcttcca cttctattcc acggagaaaa aaattgattt gtgtcacaga agttttatg 780
gaaacttagca ccatgtctac agaaactgaa ccattttgtt aaaaataaagc agcattcaag 840
aatgaagctg ctgggtttgg aggtgtcccc acggctctgc tagtgcctgc tctcctttc 900
tttgggtctg cagctggctt tggattttgc tatgtcaaaa ggtatgtgaa ggccttcct 960
tttacaaaca agaatcagca gaagggaaatg atcgaaccca aagttagtaaa ggaggagaag 1020
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aagagtccaa gcaaaactac cgtgcgtatgc ctggaaagctg aagtttagat gagacagaaa 1140
tgaggagaca cacctgaggc tgggttcttt catgctccctt accctgcccc agctgggaa 1200
atcaaaaaggc ccaaagaacc aaagaagaaa gtccacccctt ggttccataac tggaatcagc 1260

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tcaggactgc	cattggacta	tggagtgcac	caaagagaat	gcccttctcc	ttattgtAAC	1320
cctgtctgga	tccttatccctc	ctacccctcaa	agcttccac	ggccttctta	gcctggctat	1380
gtccataataa	tatcccactg	ggagaaaagga	gtttgcaaa	gtgcaaggac	ctaaaacatc	1440
tcatcagtat	ccagtggtaa	aaaggcctcc	tggctgtctg	aggcttagtg	ggttgaagc	1500
caaggagtca	ctgagaccaa	ggcttctct	actgattccg	cagctcagac	cctttctca	1560
gctctgaaag	agaaaacacgt	atcccacctg	acatgtcctt	ctgagcccg	taagagcaaa	1620
agaatggcag	aaaagttag	cccctgaaag	ccatggagat	tctcataact	tgagaccaa	1680
tctctgtaaa	gctaaaataa	agaaatagaa	caaggctgag	gatacgacag	tacactgtca	1740
gcagggactg	taaacacaga	caggtcaaa	gtgtttctc	tgaacacatt	gagttggaaat	1800
cactgttag	aacacacaca	cttactttt	ctggctctta	ccactgctga	tattttctct	1860
aggaatata	cttttacaag	taacaaaaat	aaaaactctt	ataaaattct	atttttatct	1920
gagttacaga	aatgattact	aaggaagatt	actcagtaat	ttgtttaaaa	agtaataaaa	1980
ttcaacaaac	atttgctgaa	tagctactat	atgtcaagtg	ctgtgcaagg	tattacactc	2040
tgtattgaa	tattattcct	caaaaaattg	cacatagtag	aacgctatct	gggaagctat	2100
tttttcagt	tttgcatttt	ctagtttac	tacttccaaa	ctaattttta	ttttgcgtga	2160
gactaatctt	attcattttc	tctaataatgg	caaccattat	aaccttaatt	tattattaac	2220
atacctaaga	agtacattgt	tacctctata	taccaaagca	cattttaaaa	gtgccattaa	2280
caaagtatc	actagccctc	cttttccaa	caagaaggaa	ctgagagatg	cagaatattt	2340
tgtgacaaaaa	aattaaagca	tttagaaaac	tt			2372

<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

Met	Ala	Arg	Cys	Phe	Ser	Leu	Val	Leu	Leu	Leu	Thr	Ser	Ile	Trp	Thr
1				5				10					15		

Thr	Arg	Leu	Leu	Val	Gln	Gly	Ser	Leu	Arg	Ala	Glu	Glu	Leu	Ser	Ile
				20				25					30		

Gln	Val	Ser	Cys	Arg	Ile	Met	Gly	Ile	Thr	Leu	Val	Ser	Lys	Lys	Ala
					35			40					45		

Asn	Gln	Gln	Leu	Asn	Phe	Thr	Glu	Ala	Lys	Glu	Ala	Cys	Arg	Leu	Leu
					50			55				60			

Gly	Leu	Ser	Leu	Ala	Gly	Lys	Asp	Gln	Val	Glu	Thr	Ala	Leu	Lys	Ala
					65			70			75		80		

Ser	Phe	Glu	Thr	Cys	Ser	Tyr	Gly	Trp	Val	Gly	Asp	Gly	Phe	Val	Val
					85			90					95		

Ile	Ser	Arg	Ile	Ser	Pro	Asn	Pro	Lys	Cys	Gly	Lys	Asn	Gly	Val	Gly
					100			105					110		

Val	Leu	Ile	Trp	Lys	Val	Pro	Val	Ser	Arg	Gln	Phe	Ala	Ala	Tyr	Cys
					115			120					125		

Tyr	Asn	Ser	Ser	Asp	Thr	Trp	Thr	Asn	Ser	Cys	Ile	Pro	Glu	Ile	Ile
					130			135			140				

Thr	Thr	Lys	Asp	Pro	Ile	Phe	Asn	Thr	Gln	Thr	Ala	Thr	Gln	Thr	Thr
					145			150			155		160		

Glu	Phe	Ile	Val	Ser	Asp	Ser	Thr	Tyr	Ser	Val	Ala	Ser	Pro	Tyr	Ser
					165				170				175		

Thr	Ile	Pro	Ala	Pro	Thr	Thr	Pro	Pro	Ala	Pro	Ala	Ser	Thr	Ser	
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
195 200 205
Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
210 215 220
Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
225 230 235 240
Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
245 250 255
Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
260 265 270
Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
275 280 285
Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
290 295 300
Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305 310 315 320
Glu Val

<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202
gagtttcca tccaggtgtc atgc 24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg 22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
tggagcagga ggagtagtag tagg 24

<210> 205

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Synthetic oligonucleotide probe

<400> 205

aggaggcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt

50

<210> 206

<211> 1620

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (973)..(973)

<223> a, t, c or g

<220>

<221> modified_base

<222> (977)..(977)

<223> a, t, c or g

<220>

<221> modified_base

<222> (996)..(996)

<223> a, t, c or g

<220>

<221> modified_base

<222> (1003)..(1003)

<223> a, t, c or g

<400> 206

agatggcggt cttggcacct ctaattgctc tcgtgttattc ggtgccgcga ctttcacgat 60

ggctcgccca accttactac cttctgtcgg ccctgctctc tgctgccttc ctactcgtga 120

ggaaactgcc gccgctctgc cacggctgc ccacccaacg cgaagacggg aaccctgtg 180

actttgactg gagagaagtg gagatcctga tgtttctca gtcattgtg atgatgaaga 240

accgcagatc catcaactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300

ccaacacaat tctttcttc cgctggata ttcgcatgg cctactttac atcacactct 360

gcatagtgtt cctgatgacg tgcaaaccccc ccctatataat gggcccttag tatataaagt 420

acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480

tggagttctt tgccaatttg tctaattgact gccaatcatt tgcccctatc tatgctgacc 540

tctcccttaa atacaactgt acagggctaa attttggaa ggtggatgtt ggacgctata 600

ctgatgttag tacgcggtag aaagttagca catcaccctt caccaggca ctccttaccc 660

tgatcctgtt ccaagggtggc aaggaggca tgcggcggcc acagattgac aagaaaggac 720

gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780

tataccagcg gcccaagaaa ctatcaaagg ctggagacaa tatcccttag ggcggctg 840

tggcttcaac cccaccaca gtgtcagatg gggaaaacaa gaaggataaa taagatccctc 900

actttggcag tgcttcctt cctgtcaatt ccaggcttt tccataacca caagcctgag 960

gctgcaccc ttnattnatg tttttccctt ggctgngact ggntggggca gcatgcagct 1020

tctgatttta aagaggcatc taggaatttgc tcaaggccccc tacaggaagg cctgcccattgc 1080

tgtggccaaac tgtttcaactg gagcaagaaa gagatctcat aggacggagg gggaaatgg 1140

ttccctccaa gcttgggtca gtgtttaac tgattatcg ctattcagac atctccatgg 1200

tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttgggtt 1260

agaccttagt ttaaccctaa ggtaagatgc tggggtatag aacctaaga attttcccccc 1320

aaggactctt gcttccttaa gcccttctgg cttcgtttat ggtcttcatt aaaagtataa 1380

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gccttaactt gtcgctagtc ctaaggagaa acctttaacc acaaagttt tatcattgaa 1440
 gacaatattg aacaacccccc tattttgtgg ggattgagaa ggggtgaata gaggctttag 1500
 actttcctt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560
 acatactccc cacaccaggat tgatggcttt ccgtaataaa aagattggga tttcctttg 1620

<210> 207

<211> 296

<212> PRT

<213> Homo sapiens

<400> 207

Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1 5 10 15

Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20 25 30

Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 35 40 45

Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
 260 265 270

Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
275 280 285

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208
gcttggatat tcgcatggc ctac

24

<210> 209
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209
tggagacaat atccctgagg

20

<210> 210
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210
aacagttggc cacagcatgg cagg

24

<210> 211
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211
ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212
<211> 1985
<212> DNA
<213> Homo sapiens

<400> 212
ggacagctcg cggcccccga gagctctagc cgtcgaggag ctgcctgggg acgtttgccc 60
tggggcccca gcctggcccg ggtcacccctg gcatgaggag atgggcctgt tgctcctgg 120
cccatggctc ctgctgcccc gctccctacgg actgccccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cggtcatggc aaagacctcc ttaatggagt 240

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gaagctggtg gtggagacac ccgaggagac cctgttacc taccaagggg ccagtgtat 300
 cctgcctgc cgctaccgct acgagccggc cctggctcc cgcggcgtg tgcgtgtcaa 360
 atggtgaag ctgtcgaga acggggcccc agagaaggac gtgtgggtgg ccatcggt 420
 gaggcaccgc tcctttgggg actaccaagg ccgcgtgcac ctgcggcagg acaaagagca 480
 tgacgtctcg ctggagatcc aggatctgcg gctggaggac tatgggcgtt accgctgtga 540
 ggtcattgac gggctggagg atgaaagcggt tctgggtggg ctggagctgc ggggtgtgg 600
 ctttccttac cagtcggcc acggggcgtca ccagttcaac ttccacggg gccagcagg 660
 ctgtcgagag caggctgcgg tgggtggcctc ttggagcag ctcttccggg cttgggagga 720
 gggctggac ttgtgcaacg cgggctggg gcaggatgt acggtgcagt accccatcat 780
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 cgcgcacccgc cgcctgcacc gctatgatgt attctgcttc gctactgccc tcaagggg 900
 ggtgtactac ctggagcacc ctgagaagct gacgctgaca gaggcaaggg aggcctgcca 960
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 cctggaccgc tgcgacgctg gctggctggc agatggcagc gtccgcattc ctgtggttca 1080
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 agggggcccttcc aggtgtgttacttggaca ataaatgtgt ctatgactgc cttccgccaa 1860
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1920
 aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1980
 aaaaaa 1985

<210> 213

<211> 360

<212> PRT

<213> Homo sapiens

<400> 213

Met	Gly	Leu	Leu	Leu	Leu	Val	Pro	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr
1						5						10			15

Gly	Leu	Pro	Phe	Tyr	Asn	Gly	Phe	Tyr	Tyr	Ser	Asn	Ser	Ala	Asn	Asp
					20			25			30				

Gln	Asn	Leu	Gly	Asn	Gly	His	Gly	Lys	Asp	Leu	Leu	Asn	Gly	Val	Lys
						35		40				45			

Leu	Val	Val	Glu	Thr	Pro	Glu	Glu	Thr	Leu	Phe	Thr	Tyr	Gln	Gly	Ala
					50			55			60				

Ser	Val	Ile	Leu	Pro	Cys	Arg	Tyr	Arg	Tyr	Glu	Pro	Ala	Leu	Val	Ser
65					70				75		80				

Pro	Arg	Arg	Val	Arg	Val	Lys	Trp	Trp	Lys	Leu	Ser	Glu	Asn	Gly	Ala
					85			90			95				

Pro	Glu	Lys	Asp	Val	Leu	Val	Ala	Ile	Gly	Leu	Arg	His	Arg	Ser	Phe
					100			105			110				

Gly	Asp	Tyr	Gln	Gly	Arg	Val	His	Leu	Arg	Gln	Asp	Lys	Glu	His	Asp
						115		120			125				

Val	Ser	Leu	Glu	Ile	Gln	Asp	Leu	Arg	Leu	Glu	Asp	Tyr	Gly	Arg	Tyr
130						135				140					

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
145 150 155 160

Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
165 170 175

Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
180 185 190

Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
195 200 205

Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
210 215 220

Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro
225 230 235 240

Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
245 250 255

Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu
260 265 270

His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu
275 280 285

Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys
290 295 300

Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser
305 310 315 320

Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu
325 330 335

Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr
340 345 350

Gly Val Tyr Cys Tyr Arg Gln His
355 360

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 215
ttcccttgtg ggttggag 18
<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 216
agggctggaa gccagttc 18
<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 217
agccagttag gaaatgcg 18
<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24
<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 219
gatgccacga tcgccaagggt gggacagctc tttgccgcct ggaag 45
<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
ggagagcgga gcgaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttcgttg ctactgaggc acggggccca ggggaaggca tccccagacg caggccctca 120
tggccagggg agggtgcacc aggccggccc cctgagcgcac gctcccccatt atgacgcccc 180
cgggaaacttc cagtacgacc atgaggctt cctgggacgg gaagtggcca aggaattcga 240
ccaaactcacc ccagaggaaa gccaggcccg tctggggccg atcgtggacc gcatggacc 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cgcgggggac ggcgacggct ggggtgcgt ggccgagctt cgcgctgga tcgcgcacac 360
 gcagcagcgg cacatacggg actcggtgag cgccggctgg gacacgtacg acacggaccg 420
 cgacggcgt gtgggttggg aggagctgca caacgcccacc tatggccact acgcgcccgg 480
 tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
 gcggcggttc cgggtggccg accaggatgg ggactcgatg gccactcgag aggagctgac 600
 agccttcctg caccggcagg agtccctca catgcgggac atcgtgattt ctgaaaacct 660
 ggaggacgtg gacagaaaca aagatggctt tgtccaggtt gaggagtaca tcgcggatct 720
 gtactcagcc gacggctggg aggaggagcc ggcgtgggtt cagacggaga ggcagcagtt 780
 cggggatcc cgggatctga acaaggatgg gcacctggat gggatgggg tgggcaactg 840
 ggtgctgccc cctgcccagg accagccctt ggtggaaagcc aaccacctgc tgcacgagag 900
 cgacacggac aaggatgggc ggctgagcaa agcggaaatc ctgggttaat ggaacatgtt 960
 tggggcagt caggccacca actatggca ggacctgacc cggcaccacg atgagctgtg 1020
 agcacccgcg acctgcccaca gcctcagagg cccgcacaat gaccggagga ggggcccgtg 1080
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 cagctccaaa tctgagcctc caccacatag actgaaactc ccctggccccc agccctctcc 1380
 tgcctggctt ggcctgggac acctcctctc tgccaggagg caataaaagc cagcggccggg 1440
 accttgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaa 1503

<210> 221

<211> 328

<212> PRT

<213> Homo sapiens

<400> 221

Met	Met	Trp	Arg	Pro	Ser	Val	Leu	Leu	Leu	Leu	Leu	Leu	Arg	His
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Gly	Ala	Gln	Gly	Lys	Pro	Ser	Pro	Asp	Ala	Gly	Pro	His	Gly	Gln	Gly
				20			25					30			

Arg	Val	His	Gln	Ala	Ala	Pro	Leu	Ser	Asp	Ala	Pro	His	Asp	Asp	Ala
				35			40				45				

His	Gly	Asn	Phe	Gln	Tyr	Asp	His	Glu	Ala	Phe	Leu	Gly	Arg	Glu	Val
				50			55				60				

Ala	Lys	Glu	Phe	Asp	Gln	Leu	Thr	Pro	Glu	Glu	Ser	Gln	Ala	Arg	Leu
				65			70			75			80		

Gly	Arg	Ile	Val	Asp	Arg	Met	Asp	Arg	Ala	Gly	Asp	Gly	Asp	Gly	Trp
				85			90					95			

Val	Ser	Leu	Ala	Glu	Leu	Arg	Ala	Trp	Ile	Ala	His	Thr	Gln	Gln	Arg
				100			105				110				

His	Ile	Arg	Asp	Ser	Val	Ser	Ala	Ala	Trp	Asp	Thr	Tyr	Asp	Thr	Asp
				115			120			125					

Arg	Asp	Gly	Arg	Val	Gly	Trp	Glu	Glu	Leu	Arg	Asn	Ala	Thr	Tyr	Gly
				130			135			140					

His	Tyr	Ala	Pro	Gly	Glu	Glu	Phe	His	Asp	Val	Glu	Asp	Ala	Glu	Thr
				145			150			155			160		

Tyr	Lys	Lys	Met	Leu	Ala	Arg	Asp	Glu	Arg	Arg	Phe	Arg	Val	Ala	Asp
				165			170			175					

Gln	Asp	Gly	Asp	Ser	Met	Ala	Thr	Arg	Glu	Glu	Leu	Thr	Ala	Phe	Leu
				180			185				190				

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
195 200 205

Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
210 215 220

Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225 230 235 240

Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
245 250 255

Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
260 265 270

Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
275 280 285

Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
290 295 300

Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320

Leu Thr Arg His His Asp Glu Leu
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 223

gaaatccctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 224

gtgcgcggc ctcacagctc atc

23

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 225

cccccctgag cgacgctccc ccatgatgac gcccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

ggggccttgc cttccgcact cgggcgcagc cgggtggatc tcgagcaggt gcggagcccc 60
gggcggcggg cgcggtgtcg aggatccct gacgcctctg tccctgtttc ttgtcgctc 120
ccagcctgtc tgcgtcggtt ttggcgcccc cgccctccccg cgggtgcgggg ttgcacaccc 180
atccctggct tcgctcgatt tgccgcccgg ggcgcctccca gaccttagagg ggcgcgtggcc 240
tggagcagcg ggtcgctgtgt gtcctctctc ctctgcggcg cgcccgggga tccgaagggt 300
gcggggctct gaggagggtg cgcgcggggc ctcccgacc ctggccttgc ccgcattctc 360
cctcttccc aggtgtgagc agcctatcag taccatgtc cgcgcctgg atcccggtc 420
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tctgcccagg gggctgcctt cttgaggaat tctctgtgtt tgggaacata gtatatgttt 600
ctgtatcgag catatgtggg gtcgtgtcc acaggggagt aatcagcaac tcagggggac 660
ctgtacgagt ctatagccctt cctggtcagaaaactattt ctcagtagat gccaatggca 720
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tgattgtgg aagcttaat attgggcagc gccgatttaa ttacagaag aattttgttg 960
gaaaagtggc tctaattgtt ggaattggaa cagaaggacc acatgtggc cttgttcaag 1020
ccagtaaca tcccaaaataa gaattttact tggaaaactt tacatcagcc aaagatgttt 1080
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tgggtgtgtt atttattgtt ggttggctt ctgtacatcgat cgagggagca ggcattgtgg 1260
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tccttagtaat tgcgtatcagaat gggcgttccat atgatgtatgtt ccaaggccct gcagctgctg 1860
cacatgtgc aggaatcact atcttctctg ttgtgtggc ttgggcacccctt ctggatgacc 1920
tgaaagatat ggcctttaaa ccgaaggagt tcacgcctt cttcacaaga gagttcacag 1980
gattagaacc aattgttttctt gatgtatcaga gaggcatttt tagatattt ttagaaatccc 2040
agcaataatg gtaacattttt gacaactgaa agaaaaagta caaggggatc cagtggtaa 2100
attgtattctt cataataactg aatgtcttta gcaatcata gatcatacaaa aactattaa 2160
gtatgtcaac agccatttag gcaataaagc actcctttaa agccgctgcc ttctggttac 2220
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aaa 2403

<210> 227

<211> 550

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> PRT
<213> Homo sapiens

<400> 227

Met Ser Ala Ala Trp Ile Pro Ala Leu Gly Leu Gly Val Cys Leu Leu
1 5 10 15

Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
20 25 30

Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
35 40 45

Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
50 55 60

Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
65 70 75 80

Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
85 90 95

Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
100 105 110

Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
115 120 125

Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
130 135 140

Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
145 150 155 160

Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
165 170 175

Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
180 185 190

Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
195 200 205

Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
210 215 220

Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
225 230 235 240

Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
245 250 255

Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
260 265 270

Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
275 280 285

Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
290 295 300

Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
305 310 315 320

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 229
ctgctgtcca cagggag 18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 230
ccttgaagca tactgctc 18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 231
gagatagcaa tttccgcc 18

<210> 232
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc 18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 233
cttggcacca atgtccgaga ttcc 24

<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 234
 gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg 45

<210> 235

<211> 2586

<212> DNA

<213> Homo sapiens

<400> 235
 cggccgcgtc ccgcacccgc ggccccccca ccgcgcggct cccgcacatctg caccgcgc 60
 ccggcggcct cccggcgggc gcgagcagat ccagtccggc ccgcagcgc aactcggtcca 120
 gtcggggcgg cggctgcggg cgccagagcgg agatgcagcg gcttggggcc accctgtgt 180
 gcctgtctg ggcggcgccg gtccccacgg ccccccgcgcg cgctccgacg ggcacctcgg 240
 ctccagtc aa gccccggcccg gctctcagct acccgccagga ggaggccacc ctcaatgaga 300
 tgttccgcga ggttgaggaa ctgtatggagg acacgcagca caaattgcgc agcgcgttgg 360
 aagagatgga ggcagaagaa gctgtgtcta aagcatcatc agaagtgaac ctggcaaact 420
 tacctcccag ctatcacaat gagaccaaca cagacacgaa ggttggaaat aataccatcc 480
 atgtgcaccc agaaattcac aagataacca acaaccagac tggacaaatg gtctttcag 540
 agacagttat cacatctgtg ggagacgaag aaggcagaag gagccacgag tgcatcatc 600
 acgaggactg tggggccagc atgtactgcc agtttgcctag cttccagtac acctgcccagc 660
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 tggatgttttcc aggtgtcatg gactgttgcc accatgtatt catccagat tcttaaagtt 2460
 taaagggtca catgattgtta taagcatgtt ttctttgagt tttaaattat gtataaacat 2520
 aagttgcatt tagaaatcaa gcataaaatca cttcaactgc aaaaaaaaaa aaaaaaaaaa 2580
 aaaaaaaaaa 2586

<210> 236

<211> 350

<212> PRT

<213> Homo sapiens

<400> 236

Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala

1

5

10

15

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30

Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95

Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His
100 105 110

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Gly Glu
325 330 335

Pro Ala Ala Ala Ala Ala Leu Leu Gly Gly Glu Glu Ile
340 345 350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 237
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 237
ggagctgcac cccttgc 17

<210> 238
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 238
ggaggactgt gccaccatga gagactttc aaacccaagg caaaattgg 49

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 239
gcagagcgg aatgcagcgg cttg 24

<210> 240
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 240
ttggcagctt catggagg 18

<210> 241
<211> 18
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu
 110 115 120
 Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His
 125 130 135
 Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His
 140 145 150
 Asn Gln Leu Tyr Arg Ile Ala Pro Arg Ala Phe Ser Gly Leu Ser
 155 160 165
 Asn Leu Leu Arg Leu His Leu Asn Ser Asn Leu Leu Arg Ala Ile
 170 175 180
 Asp Ser Arg Trp Phe Glu Met Leu Pro Asn Leu Glu Ile Leu Met
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 Ile Gly Gly Asn Lys Val Asp Ala Ile Leu Asp Met Asn Phe Arg
 200 205 210
 Pro Leu Ala Asn Leu Arg Ser Leu Val Leu Ala Gly Met Asn Leu
 215 220 225
 Arg Glu Ile Ser Asp Tyr Ala Leu Glu Gly Leu Gln Ser Leu Glu
 230 235 240
 Ser Leu Ser Phe Tyr Asp Asn Gln Leu Ala Arg Val Pro Arg Arg
 245 250 255
 Ala Leu Glu Gln Val Pro Gly Leu Lys Phe Leu Asp Leu Asn Lys
 260 265 270
 Asn Pro Leu Gln Arg Val Gly Pro Gly Asp Phe Ala Asn Met Leu
 275 280 285
 His Leu Lys Glu Leu Gly Leu Asn Asn Met Glu Glu Leu Val Ser
 290 295 300
 Ile Asp Lys Phe Ala Leu Val Asn Leu Pro Glu Leu Thr Lys Leu
 305 310 315
 Asp Ile Thr Asn Asn Pro Arg Leu Ser Phe Ile His Pro Arg Ala
 320 325 330
 Phe His His Leu Pro Gln Met Glu Thr Leu Met Leu Asn Asn Asn
 335 340 345
 Ala Leu Ser Ala Leu His Gln Gln Thr Val Glu Ser Leu Pro Asn
 350 355 360
 Leu Gln Glu Val Gly Leu His Gly Asn Pro Ile Arg Cys Asp Cys
 365 370 375
 Val Ile Arg Trp Ala Asn Ala Thr Gly Thr Arg Val Arg Phe Ile
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 410 415 420
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 425 430 435
 Ala Ser Gly Glu Ser Met Val Leu His Cys Arg Ala Leu Ala Glu
 440 445 450
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 455 460 465
 Thr Pro Ala His Ala Gly Arg Arg Tyr Arg Val Tyr Pro Glu Gly
 470 475 480
 Thr Leu Glu Leu Arg Arg Val Thr Ala Glu Glu Ala Gly Leu Tyr
 485 490 495
 Thr Cys Val Ala Gln Asn Leu Val Gly Ala Asp Thr Lys Thr Val
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 Ser Val Val Val Gly Arg Ala Leu Leu Gln Pro Gly Arg Asp Glu
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 Gly Gln Gly Leu Glu Leu Arg Val Gln Glu Thr His Pro Tyr His
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 Ala Leu Ala Arg Leu Pro Arg Gly Thr His Ser Tyr Asn Ile Thr
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 Arg Leu Leu Gln Ala Thr Glu Tyr Trp Ala Cys Leu Gln Val Ala
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 Phe Ala Asp Ala His Thr Gln Leu Ala Cys Val Trp Ala Arg Thr
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 Lys Glu Ala Thr Ser Cys His Arg Ala Leu Gly Asp Arg Pro Gly
 620 625 630
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 Gly Arg Arg Pro Leu Pro Pro Ala Trp Ala Phe Trp Gly Trp Ser
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<223> Synthetic Oligonucleotide Probe

<400> 246

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

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<210> 248

<211> 45

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<223> Synthetic Oligonucleotide Probe

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<211> 3401

<212> DNA

<213> Homo Sapien

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<212> PRT

<213> Homo Sapien

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Page 126

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

1

5

10

15

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Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe
 50 55 60

Tyr Ile Ser Leu Val Ile Phe Tyr Gly Leu Ile Cys Met Tyr Thr
 65 70 75

Leu Trp Trp Met Leu Arg Arg Ser Leu Lys Lys Tyr Ser Phe Glu
 80 85 90

Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys
 95 100 105

Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro
 110 115 120

Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu
 125 130 135

Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp
 140 145 150

Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu
 155 160 165

Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp
 170 175 180

Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val
 185 190 195

Thr Ile Pro Pro Ser Ile Ala Gln Leu Thr Gly Leu Lys Glu Leu
 200 205 210

Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala
 215 220 225

Phe Leu Arg Glu Asn Leu Arg Ala Leu His Ile Lys Phe Thr Asp
 230 235 240

Ile Lys Glu Ile Pro Leu Trp Ile Tyr Ser Leu Lys Thr Leu Glu
 245 250 255

Glu Leu His Leu Thr Gly Asn Leu Ser Ala Glu Asn Asn Arg Tyr
 260 265 270

Ile Val Ile Asp Gly Leu Arg Glu Leu Lys Arg Leu Lys Val Leu
 275 280 285

Arg Leu Lys Ser Asn Leu Ser Lys Leu Pro Gln Val Val Thr Asp
 290 295 300

Val Gly Val His Leu Gln Lys Leu Ser Ile Asn Asn Glu Gly Thr
 305 310 315

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr
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Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser
 335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn
 350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ser Phe Gln His Leu His
 365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
 380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
 395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
 410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
 425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
 440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
 455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
 470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
 485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
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Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
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Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<400> 253

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<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

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ggcttcaggg cggtccagggc ggttctagca ctggatttg 300

aaactttgag cccttgacag tgatctaaa ccacggaaaa ccacctggct 350

ccaggctgcc agtctcctat ttgtggataa tcccgtggc actgggtca 400

gttatgtcaa tggtagtggt gcctatgcca aggacctggc tatggtg 450

tcagacatga tggttctcct gaagaccttc ttca gttgcc acaaagaatt 500

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aagacaaagg tctggcagag gtgtctaagg ttgcagagca agtactgaat 750

gccgtaaata aggggctcta cagagaggcc acagagctgt gggggaaagc 800

agaaatgatc attgaacaga acacagatgg ggtgaacttc tataacatct 850

taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900

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agatgcctta agccagctca tgaatggccc catcagaag aagctcaaaa 1000

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ttattcctga ggatcaatcc tggggaggcc aggctaccaa cgtctttgtg 1050
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gctggaggca gggatcaacg tgacggtgta taatggacag ctggatctca 1150
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gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250
taaatcttg gaaacatctg ctttgcataa gtcctacaag aaccttgctt 1300
tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
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gggctggaga ttagctgggtt tggccttggg gcacagagct gagctgaggc 1450
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gatcaagaag gttctgacca gcttctgcag aggataaaat cattgtctct 1550
ggaggcaatt tggaaattat ttctgcttct taaaaaaaaacc taagatttt 1600
aaaaaaaaattg atttgttttg atcaaaataa aggatgataa tagatattaa 1650

<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

Met Glu Leu Ala Leu Arg Arg Ser Pro Val Pro Arg Trp Leu Leu
1 5 10 15

Leu Leu Pro Leu Leu Leu Gly Leu Asn Ala Gly Ala Val Ile Asp
20 25 30

Trp Pro Thr Glu Glu Gly Lys Glu Val Trp Asp Tyr Val Thr Val
35 40 45

Arg Lys Asp Ala Tyr Met Phe Trp Trp Leu Tyr Tyr Ala Thr Asn
50 55 60

Ser Cys Lys Asn Phe Ser Glu Leu Pro Leu Val Met Trp Leu Gln
65 70 75

Gly Gly Pro Gly Gly Ser Ser Thr Gly Phe Gly Asn Phe Glu Glu
80 85 90

Ile Gly Pro Leu Asp Ser Asp Leu Lys Pro Arg Lys Thr Thr Trp
95 100 105

Leu Gln Ala Ala Ser Leu Leu Phe Val Asp Asn Pro Val Gly Thr
110 115 120

Gly Phe Ser Tyr Val Asn Gly Ser Gly Ala Tyr Ala Lys Asp Leu
125 130 135

Ala Met Val Ala Ser Asp Met Met Val Leu Leu Lys Thr Phe Phe
140 145 150

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly
 305 310 315
 Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp
 320 325 330
 Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe
 335 340 345
 Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly
 350 355 360
 Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp
 365 370 375
 Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu
 380 385 390
 Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp
 395 400 405
 Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn
 410 415 420
 Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser
 425 430 435
 Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln
 440 445 450

Gln Glu

<210> 256

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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tgctgctggc tcgggctgga ctcaggaagc cggagtcgca ggaggcggcg 100
ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200
tgtggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctggca 250
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cgggtggatg gtccagtttgc ccagctgac ttccatgcca tccttctgga 350
gcctgcaggc ctactacacc cgttacttcg tatcgaatat ctatctgagc 400
cctcgctacc tgggaaattc accctatgac attgccttgg tgaagctgac 450
tgcacctgtc acctacacta aacacatcca gcccacatgt ctccaggcct 500
ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550
tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600
tcaggtcgcc atcataaaca actctatgtc caaccaccc ttcctcaagt 650
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tttggatggaa tccagaagct gatggccag agtggcatgt cccagccaga 900
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tggggccggc ctgagcctac ctgagccat gcagcctggg gccactgcca 1000
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ttgatgcctt gcagggcatt cttcaaaaaaa aaaaaaaaaa aaaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg
1 5 10 15

Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

20

25

30

Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60
Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75
Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90
Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
95 100 105
Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
110 115 120
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
125 130 135
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140 145 150
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
155 160 165
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
170 175 180
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
185 190 195
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
200 205 210
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
215 220 225
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
230 235 240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
245 250 255
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260 265 270
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
275 280 285
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
290 295 300
Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
305 310

<210> 258

<211> 2427

<212> DNA

<213> Hómo Sapien

<400> 258

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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cgtgcggacc ctgaggaaga gctgagtctc accttgccc tgagacagca 200
gaatgtggaa agactctcg agctggtgca ggctgtgtcg gatcccagct 250
ctcctcaata cgaaaaatac ctgaccctag agaatgtggc tgatctggt 300
aggccatccc cactgaccct ccacacggtg caaaaatggc tcttggcagc 350
cgagccccag aagtgcatt ctgtgatcac acaggacttt ctgacttgct 400
ggctgagcat ccgacaagca gagctgctgc tccctgggc tgagtttcat 450
caatatgtgg gaggacctac ggaaacccat gttgtaaggt ccccacatcc 500
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gtgacaggga ctgtaggcct gcatctgggg gtaacccct ctgtgatccg 650
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tgatggctac tgggtggta gcaacagagt gcccattcca tgggtgtccg 1450
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gagcacagga tccttagtgg ccggcccccctt cttggctttc tcaacccaag 1550
gctctaccag cagcatgggg caggtctctt tgatgtaacc cgtggctgcc 1600

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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gtcccccgtcc ctgaagctgg cagttcagtc ccttattctg ccctgttgaa 1800
agccctgctg aaccctcaac tattgactgc tgcagacagc ttatctccct 1850
aaccctgaaa tgctgtgagc ttgacttgac tcccaaccct accatgctcc 1900
atcatactca ggtctcccta ctccgcctt agattcctca ataagatgct 1950
gtaaactagca tttttgaat gcctctccct ccgcatactca tctttctctt 2000
ttcaatcagg cttttccaaa ggggtgtata cagactctgt gcactatttc 2050
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tttactctt cctaccctga catccagaaa caatggcctc cagtgcatac 2150
ttctcaatct ttgctttatg gcctttccat catagttgcc cactccctct 2200
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aatgattgat acctcaaatg taaaaaa 2427

<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Ser Gly Lys Cys Ser Tyr Ser Pro Glu Pro Asp Gln Arg Arg Thr
20 25 30

Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
35 40 45

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
50 55 60

Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln
65 70 75

Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg
80 85 90

Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala
95 100 105

Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu
110 115 120

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Cys Trp Leu Ser Ile Arg Gln Ala Glu Leu Leu Leu Pro Gly
 125 130 135
 Ala Glu Phe His His Tyr Val Gly Gly Pro Thr Glu Thr His Val
 140 145 150
 Val Arg Ser Pro His Pro Tyr Gln Leu Pro Gln Ala Leu Ala Pro
 155 160 165
 His Val Asp Phe Val Gly Gly Leu His Arg Phe Pro Pro Thr Ser
 170 175 180
 Ser Leu Arg Gln Arg Pro Glu Pro Gln Val Thr Gly Thr Val Gly
 185 190 195
 Leu His Leu Gly Val Thr Pro Ser Val Ile Arg Lys Arg Tyr Asn
 200 205 210
 Leu Thr Ser Gln Asp Val Gly Ser Gly Thr Ser Asn Asn Ser Gln
 215 220 225
 Ala Cys Ala Gln Phe Leu Glu Gln Tyr Phe His Asp Ser Asp Leu
 230 235 240
 Ala Gln Phe Met Arg Leu Phe Gly Gly Asn Phe Ala His Gln Ala
 245 250 255
 Ser Val Ala Arg Val Val Gly Gln Gln Gly Arg Gly Arg Ala Gly
 260 265 270
 Ile Glu Ala Ser Leu Asp Val Gln Tyr Leu Met Ser Ala Gly Ala
 275 280 285
 Asn Ile Ser Thr Trp Val Tyr Ser Ser Pro Gly Arg His Glu Gly
 290 295 300
 Gln Glu Pro Phe Leu Gln Trp Leu Met Leu Leu Ser Asn Glu Ser
 305 310 315
 Ala Leu Pro His Val His Thr Val Ser Tyr Gly Asp Asp Glu Asp
 320 325 330
 Ser Leu Ser Ser Ala Tyr Ile Gln Arg Val Asn Thr Glu Leu Met
 335 340 345
 Lys Ala Ala Ala Arg Gly Leu Thr Leu Leu Phe Ala Ser Gly Asp
 350 355 360
 Ser Gly Ala Gly Cys Trp Ser Val Ser Gly Arg His Gln Phe Arg
 365 370 375
 Pro Thr Phe Pro Ala Ser Ser Pro Tyr Val Thr Thr Val Gly Gly
 380 385 390
 Thr Ser Phe Gln Glu Pro Phe Leu Ile Thr Asn Glu Ile Val Asp
 395 400 405
 Tyr Ile Ser Gly Gly Phe Ser Asn Val Phe Pro Arg Pro Ser
 410 415 420
 Tyr Gln Glu Glu Ala Val Thr Lys Phe Leu Ser Ser Ser Pro His
 425 430 435

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Pro Pro Ser Ser Tyr Phe Asn Ala Ser Gly Arg Ala Tyr Pro
440 445 450
Asp Val Ala Ala Leu Ser Asp Gly Tyr Trp Val Val Ser Asn Arg
455 460 465
Val Pro Ile Pro Trp Val Ser Gly Thr Ser Ala Ser Thr Pro Val
470 475 480
Phe Gly Gly Ile Leu Ser Leu Ile Asn Glu His Arg Ile Leu Ser
485 490 495
Gly Arg Pro Pro Leu Gly Phe Leu Asn Pro Arg Leu Tyr Gln Gln
500 505 510
His Gly Ala Gly Leu Phe Asp Val Thr Arg Gly Cys His Glu Ser
515 520 525
Cys Leu Asp Glu Glu Val Glu Gly Gln Gly Phe Cys Ser Gly Pro
530 535 540
Gly Trp Asp Pro Val Thr Gly Trp Gly Thr Pro Thr Ser Gln Leu
545 550 555
Cys

<210> 260
<211> 1638
<212> DNA
<213> Homo Sapien

<400> 260
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attccagggc tcctcttcct tctttttt ctgctctgtg ctgttggca 100
agtgagccct tacagtgc 50
cctggaaacc cacttggcct gcataccg 150
tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 200
ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 250
taagggact ccactgccc 50
cttacgaaga ggccaagcaa tatctgtctt 300
atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggc 350
tacatcctca gcagtagtgg agatgggc 50
caacaccgag actcagggtc 400
ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcagg 450
tcagcatttt tggaaaggac ttccctgctca actacccttt ctcaacatca 500
gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 550
cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 600
cccagaagct tcgagtggc 50
ttcctaaagc ccaagttaa agatggtggt 650
cgagggcca acgactccac ttcatccatg cccgagcaga taaaattca 700
750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaaggca 800
atgccaatga catcgccatg gattatgatt atgccctcct ggaactcaaa 850
aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctccgtctaa 900
gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950
caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000
ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctgggt 1050
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gatttcaacg tggctgtcag aatcaactcct ctcaaataatg cccagattt 1200
ctattggatt aaaggaaact acctggattt tagggagggg tgacacagt 1250
ttccctcctg gcagcaatta agggcttca ttttcttatt ttaggagagg 1300
ccaaattgtt ttttgcatt ggcgtgcaca cgtgtgtgtg ttttgcatt 1350
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caaactttga ttttatttc atctgaactt gtttcaaaga tttatattaa 1600
atattggca tacaagagat atgaaaaaaa aaaaaaaa 1638

<210> 261

<211> 383

<212> PRT

<213> Homo Sapien

<400> 261

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu
1 5 10 15

Cys Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro
20 25 30

Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
35 40 45

Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
50 55 60

Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
65 70 75

Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
80 85 90

Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile

95

100

105

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ser Ser Ser Gly Asp Gly Ala Gln His Arg Asp Ser Gly Ser
110 115 120
Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly Tyr Asp Ser
125 130 135
Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr Pro Phe
140 145 150
Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu Val
155 160 165
Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
170 175 180
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu
185 190 195
Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr
200 205 210
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys
215 220 225
Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
230 235 240
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro
245 250 255
His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys
260 265 270
Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp
275 280 285
Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu
290 295 300
Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala
305 310 315
Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln Gln
320 325 330
Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp
335 340 345
Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg
350 355 360
Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly
365 370 375
Asn Tyr Leu Asp Cys Arg Glu Gly
380

<210> 262

<211> 1378

<212> DNA

<213> Homo Sapien

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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caggataacct gttcccccag cctgtggaa gccccagcag ctgaaccggg 200
ttgtggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca ccactgcgca ggttctctgc tcaccagccg 300
ctgggtgatc actgctgccc actgttcaa ggacaacctg aacaaaccat 350
acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctgcagcgct 500
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550
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ggagcgggat gcttgtctgg gcgactccgg gggcccccctc atgtgccagg 800
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catcaggccc cgcccaacgg cctcatgtcc cgcggccac gacttccggc 1250
cccgcccccg ggccccagcg ctttgtgtataaaatgtt aatgattttt 1300
ataggtatTT gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
ataaaattatt tattctccaa aaaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Met Val Val Ser Gly Ala Pro Pro Ala Leu Gly Gly Gly Cys Leu
1 5 10 15

Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu
20 25 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln
35 40 45

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu
50 55 60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys
65 70 75

Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His
80 85 90

Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu
95 100 105

Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys
110 115 120

Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
125 130 135

Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser
140 145 150

Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala
155 160 165

Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
170 175 180

Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
185 190 195

Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
200 205 210

Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
215 220 225

Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
230 235 240

Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
245 250 255

Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
260 265 270

Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
275 280 285

Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
290 295 300

Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
305 310 315

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

gtccgcaagg atgcctacat gttc 24

<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagaggtgt ctaaggttg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgccccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>
<223> Synthetic Oligonucleotide Probe

<400> 269
gaatgccctg caagcatcaa ctgg 24

<210> 270
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 270
gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 271
gcgaaaggc agaatggac tccaaag 26

<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 272
cagccctgcc acatgtgc 18

<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 273
tactgggtgg tcagcaac 18

<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 274
ggcgaagagc agggtgagac cccg 24

<210> 275
<211> 45

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
gccctcatcc tctctggcaa atgcagttac agcccgagc ccgac 45

<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
ggcaggat tccagggctc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatgcatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 280

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
ttacagtgcc ccctggaaac ccacttggcc tgcataaccgc ctccc 45

<210> 281
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 281
cgtctcgagc gctccataca gttcccttgc ccca 34

<210> 282
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 282
tggaggggga gcgggatgct tgtctggcg actccggggg cccccctcatg 50
tgccaggtgg a 61

<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 283
ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50
gcagccatct gtactggcg ggagcaggac agggaccat cactgaggac 100
atgctgtgtg ccggctact 119

<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien

<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50
ccgctactgc tactgctggt ggccaccaca ggccccgttggagc 100
agatgaggag aaacgttga tggggagact gcacaaccc 150
aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200
ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250
caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300
gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350
tacaacctca gcgccgcccac ctgcagccca ggccagatgt gcggccacta 400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cacgcaggtg gtatggcca agacagagag gatcggtgt ggttccact 450
tctgtgagaa gctccaggg gttgaggaga ccaacatcga attactggtg 500
tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
ggggactccg tgctccaat gtccctctgg ctaccactgc aagaactccc 600
tctgtgaacc catcggaaagc ccggaaagatg ctcaggattt gccttacctg 650
gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700
aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750
cagaggtctc aggctccctg gcaaccaagg ctctgcctgc tgtggaaacc 800
caggccccaa cttccttagc aacgaaagac ccgcctcca tggcaacaga 850
ggctccacct tgctgtacaa ctgaggtccc ttccattttg gcagctcaca 900
gcctgcccctc cttggatgag gagccagtta cttcccaa atcgacccat 950
gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000
ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050
caagggact cttacccat gcccaggagg aggctgaggc tgaggctgag 1100
ttgcctcctt ccagtgaggt cttggcctca gttttccag cccaggacaa 1150
gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200
agtcctgccc caattcccc aatacctctg ccaccgctaa tgccacgggt 1250
gggcgtcccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300
caagcctagc gttgtgtcag ggctgaactc gggccctggt catgtgtggg 1350
gccctctcct gggactactg ctcctgcctc ctctggtgtt ggctggaatc 1400
ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtccctctgt 1450
catttcccc accctgtccc cagcccccaa acaagatact tcttggtaa 1500
ggccctccgg aaggaaagg ctacggggca tgtgcctcat cacaccatcc 1550
atcctggagg cacaaggcct ggctggctgc gagctcagga ggccgcctga 1600
ggactgcaca ccgggcccac acctctcctg cccctccctc ctgagtcctg 1650
ggggtggag gatttgaggg agctcactgc ctacctggcc tggggctgtc 1700
tgcccacaca gcatgtgcgc tctccctgag tgcctgtgt a gctggggatg 1750
gggattccta gggcagatg aaggacaagc cccactggag tggggttctt 1800
tgagtgggg aggcaaggac gagggagga aagtaactcc tgactctcca 1850
ataaaaacct gtccaaacctg tgaaa 1875

<210> 285
<211> 463
<212> PRT

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo Sapien

<400> 285

Met	His	Gly	Ser	Cys	Ser	Phe	Leu	Met	Leu	Leu	Leu	Pro	Leu	Leu	
1				5				10					15		
Leu	Leu	Leu	Val	Ala	Thr	Thr	Gly	Pro	Val	Gly	Ala	Leu	Thr	Asp	
			20				25					30			
Glu	Glu	Lys	Arg	Leu	Met	Val	Glu	Leu	His	Asn	Leu	Tyr	Arg	Ala	
				35				40				45			
Gln	Val	Ser	Pro	Thr	Ala	Ser	Asp	Met	Leu	His	Met	Arg	Trp	Asp	
			50				55				60				
Glu	Glu	Leu	Ala	Ala	Phe	Ala	Lys	Ala	Tyr	Ala	Arg	Gln	Cys	Val	
			65				70				75				
Trp	Gly	His	Asn	Lys	Glu	Arg	Gly	Arg	Arg	Gly	Glu	Asn	Leu	Phe	
			80				85				90				
Ala	Ile	Thr	Asp	Glu	Gly	Met	Asp	Val	Pro	Leu	Ala	Met	Glu	Glu	
			95				100				105				
Trp	His	His	Glu	Arg	Glu	His	Tyr	Asn	Leu	Ser	Ala	Ala	Thr	Cys	
			110				115				120				
Ser	Pro	Gly	Gln	Met	Cys	Gly	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	
			125				130				135				
Lys	Thr	Glu	Arg	Ile	Gly	Cys	Gly	Ser	His	Phe	Cys	Glu	Lys	Leu	
			140				145				150				
Gln	Gly	Val	Glu	Glu	Thr	Asn	Ile	Glu	Leu	Leu	Val	Cys	Asn	Tyr	
			155				160				165				
Glu	Pro	Pro	Gly	Asn	Val	Lys	Gly	Lys	Arg	Pro	Tyr	Gln	Glu	Gly	
			170				175				180				
Thr	Pro	Cys	Ser	Gln	Cys	Pro	Ser	Gly	Tyr	His	Cys	Lys	Asn	Ser	
			185				190				195				
Leu	Cys	Glu	Pro	Ile	Gly	Ser	Pro	Glu	Asp	Ala	Gln	Asp	Leu	Pro	
			200				205				210				
Tyr	Leu	Val	Thr	Glu	Ala	Pro	Ser	Phe	Arg	Ala	Thr	Glu	Ala	Ser	
			215				220				225				
Asp	Ser	Arg	Lys	Met	Gly	Thr	Pro	Ser	Ser	Leu	Ala	Thr	Gly	Ile	
			230				235				240				
Pro	Ala	Phe	Leu	Val	Thr	Glu	Val	Ser	Gly	Ser	Leu	Ala	Thr	Lys	
			245				250				255				
Ala	Leu	Pro	Ala	Val	Glu	Thr	Gln	Ala	Pro	Thr	Ser	Leu	Ala	Thr	
			260				265				270				
Lys	Asp	Pro	Pro	Ser	Met	Ala	Thr	Glu	Ala	Pro	Pro	Cys	Val	Thr	
			275				280				285				
Thr	Glu	Val	Pro	Ser	Ile	Leu	Ala	Ala	His	Ser	Leu	Pro	Ser	Leu	
			290				295				300				

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
305 310 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
320 325 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
335 340 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
350 355 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
365 370 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
380 385 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 286

tcctgcagtt tcctgatgc 19

<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 288 atgaggagaa acgtttgatg gtggagctgc acaacctcta ccggg 45
<210> 289
<211> 3662
<212> DNA
<213> Homo Sapien
<400> 289
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tcattctcca agttatggtg gacgtacttc tggatgttctc cctctgcttg 100
cttttcaca ttagcagacc ggacttaagt cacaacagat tttttcat 150
caaggcaagt tccatgagcc accttcaaag cttcgagaa gtgaaactga 200
acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaa 250
attacacttc tctccttggc tggaaacagg attgttggaa tactccctga 300
acatctgaaa gagtttca 350
atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400
tatctcaaca gcaaccgagt cacatcaatg gaacctgggt atttgacaa 450
tttggccaac acactccttgc tggatgttca 500
ctatcccacc caagatgtt aaactgcccc aactgcaaca tctcgaattt 550
aaccgaaaca agattaaaaa tggatgttca 600
tgctctgaag tctctgaaa tgcaaaagaaa tggatgttca 650
atggagcttt ttggggctg agcaacatgg aaattttgca gctggaccat 700
aacaacctaa cagagattac caaaggctgg ctttacggct tgctgtatgc 750
gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800
cctgggagtt ctgccagaag ctcagtggc tggaccta 850
ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900
actgcacatt gggaaacaaca gagtcagcta cattgctgat tggcccttcc 950
gggggcttcc cagttaaag acttggatc tggatgttca 1000
tggactattt aagacatgaa tggatgttcc tctgggcttgc acaaactgag 1050
gcgactgata ctccaaggaa atcggatccg ttcttattact aaaaaggct 1100
tcactggttt ggatgcattt gggatgttgc acctgatgttca 1150
atgtcttac aaggcaatgc attttcacaa atgaagaaac tggatgttca 1200
gcatttaat acatcaagcc ttttgcgttca tggccagcttca 1250
cacagtgggt ggcggaaaac aactttcaga gctttgttca 1300
gcccatcctc agctgcttca 1350
aggaagaagc attttgcgttca ttagccaga

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tggcttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400
aaacacagtc ggcaataaaa gggttccaatt tgagttcat ctgctcagct 1450
gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500
actactgcat gatgctgaaa tggaaaatta tgcacaccc tcggcccaag 1550
gtggcgaggt gatggagttt accaccatcc ttccggctgcg cgaggtggaa 1600
tttgcctgtg agggaaata tcagtgtgtc atctccaatc actttggttc 1650
atcctactct gtcaaagcca agcttacagt aaatatgtt ccctcattca 1700
ccaagacccc catggatctc accatccgag ctggggccat ggcacgcctg 1750
gagtgctgctg ctgtggggca cccagcccc cagatagcct ggcagaagga 1800
tggggcaca gacttcccag ctgcacggga gagacgcgtg catgtgtgc 1850
ccgaggatga cgtgttctt atcgtggatg tgaagataga ggacattggg 1900
gtatacagct gcacagctca gaacagtgc ggaagtattt cagcaaatgc 1950
aactctgact gtcctagaaa caccatcatt tttgcggcca ctgttggacc 2000
gaactgtaac caagggagaa acagccgtcc tacagtgcatt tgctggagga 2050
agccctcccc ctaaactgaa ctggaccaaa gatgatagcc cattgggtgt 2100
aaccgagagg cactttttt cagcaggcaa tcagttctg attattgtgg 2150
actcagatgt cagtgtatgtc gggaaataca catgtgagat gtctaacacc 2200
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ccactgtggg tgtcgtgtatcc atagccgtgg tttgctgtgt ggtggcacc 2350
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gttatttgc atctcaggaa acgttagctg acaggcagga tgggtacgtg 2500
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atttttctt ccacaacatg acagtagtgg gacctgccat attgacaata 2600
gcagtgaagc tgatgtggaa gctgccacag atctgttcc ttgtccgttt 2650
ttgggatcca caggccctat gtatttgaag ggaaatgtgt atggctcaga 2700
tcctttgaa acatatcata caggttgcag tcctgaccca agaacagttt 2750
taatggacca ctatgagccc agttacataa agaaaaagga gtgctaccca 2800
tgttctcatc cttcagaaga atcctgcgaa cggagcttca gtaatatac 2850
gtggccctca catgtgagga agctacttaa cactagttac tctcacaatg 2900
aaggacctgg aatgaaaaat ctgtgtctaa acaagtccctc ttttagatttt 2950

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

agtgcaaatc cagagccagc gtcgggtgcc tcgagtaatt ctttcatggg 3000
tacctttgga aaagctctca ggagacctca cctagatgcc tattcaagct 3050
ttggacagcc atcagattgt cagccaagag ccttttattt gaaagctcat 3100
tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150
agattttcag gaagaaaatc acatttgtac ctttaaacag acttttagaaa 3200
actacaggac tccaaattt cagtcttatg acttggacac atagactgaa 3250
tgagacaaa gggaaagctt aacatactac ctcaagtgaa cttttatata 3300
aaagagagag aatcttatgt tttttaatg gagttatgaa ttttaaaagg 3350
ataaaaaatgc ttttattata cagatgaacc aaaattacaa aaagttatga 3400
aaatttttat actggaaatg atgctcatat aagaataacct ttttaaacta 3450
tttttaact ttgtttatg caaaaaagta tcttacgtaa attaatgata 3500
taaatcatga ttatttatg tattttata atgccagatt tcttttatg 3550
gaaaatgagt tactaaagca ttttaataa tacctgcctt gtaccatttt 3600
ttaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650
tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

Met Val Asp Val Leu Leu Leu Phe Ser Leu Cys Leu Leu Phe His
1 5 10 15

Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
35 40 45

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
50 55 60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
65 70 75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
80 85 90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
95 100 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
110 115 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
125 130 135

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
140 145 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
155 160 165

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
170 175 180

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
185 190 195

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
200 205 210

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
215 220 225

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
230 235 240

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
245 250 255

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
260 265 270

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn
275 280 285

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
290 295 300

Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
305 310 315

Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
320 325 330

Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
335 340 345

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
350 355 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
365 370 375

Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
380 385 390

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
395 400 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
410 415 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
425 430 435

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
440 445 450

Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
455 460 465
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
470 475 480
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
485 490 495
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
500 505 510
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
515 520 525
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
530 535 540
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
545 550 555
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
560 565 570
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
575 580 585
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val
590 595 600
Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
605 610 615
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
620 625 630
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
635 640 645
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
650 655 660
Gly Gly Ser Pro Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
665 670 675
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
680 685 690
Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
695 700 705
Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
710 715 720
Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
725 730 735
Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
740 745 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
 1025 1030 1035
 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
 1040 1045 1050
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
 1055

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 291
<211> 2906
<212> DNA
<213> Homo Sapien

<400> 291
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ggctgttggg tgccttgaa aaatgaagga tgcaggacgc agcttctcc 100
tggAACGAA cgcaatggat aaactgattt tgcaagagag aaggaagaac 150
gaagctttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
acacaggag cattcaagaa taaaataaac cagagttaga cccgcgggg 250
ttggtgtgtt ctgacataaa taaataatct taaagcagct gttccctcc 300
ccaccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacaa 350
agaaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
gatatttttgaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
ggtgtgggtgg tgtttcctt tcttttgaa tttcccacaa gaggagagga 500
aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
gcagattgag gcattgattt ggggagagaa accagcagag cacagttgga 600
tttgcctta tggtgactaa aattgacgga taattgcagt tggattttc 650
ttcatcaacc tcctttttt taaatttta ttccctttgg tatcaagatc 700
atgcgttttcttgcctt aaccacctgg atttccatct ggatgttgct 750
gtgatcagtc taaaatacaa ctgttgaat tccagaagga ccaacaccag 800
ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
ataggcctta ggttaacag ggccttattt gacccctgc ttgtggtgct 900
gctggctctt caacttcttg tggtggctgg tctggcgcgg gctcagacct 950
gcccttctgt gtgcctcgtc agcaaccagt tcagcaaggt gatttgtgtt 1000
cgaaaaacc tgcgtgaggt tccggatggc atctccacca acacacggct 1050
gctgaacctc catgagaacc aaatccagat catcaaagt aacagctca 1100
agcacttgag gcacttggaa atcctacagt tgagtaggaa ccatatcaga 1150
accattgaaa ttggggctt caatggcttg gcaacacctca acactctgg 1200
actctttgac aatcgctta ctaccatccc gaatggagct tttgtatact 1250
tgtctaaact gaaggagctc tggttgcgaa acaacccat tgaaagcatc 1300
ccttctttagt cttaacag aattccttct ttgcgccgac tagacttagg 1350
ggaattgaaa agactttcat acatctcaga aggtgcctt gaaggctgt 1400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tttatctgcc atcaggcctg gctttcca gggtttgcac caccccaaa 1550
aactgtggat gatacagtcc cagattcaag tgattgaacg gaatgcctt 1600
gacaacccctc agtcaactgt ggagatcaac ctggcacaca ataatcta 1650
attactgcct catgacccctc tcactccctt gcatcatcta gagcggatac 1700
atttacatca caacccttgg aactgttaact gtgacatact gtggctcagc 1750
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taacactcct cccaatctaa aggggaggtt cattggagag ctcgaccaga 1850
attacttcac atgctatgct ccggtgattt tggagcccc tgcagaccc 1900
aatgtcaactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950
cctgacatct gtatcttggaa ttactccaaa tggAACAGTC atgacacatg 2000
gggcgtacaa agtgcggata gctgtgctca gtgatggtac gttaaatttc 2050
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ccactactcc tttcttttac tttcaaccg tcacagttaga gactatggaa 2200
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agtggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400
tgggtttt gtggccatca cactcatggc tgcagtgtat ctggtcattt 2450
tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaaca 2500
aggactgttggaaatttataa tgtggatgtt gagattacgg gagacacacc 2550
catggaaagc cacctgccc tgcctgctat cgagcatgag cacctaaatc 2600
actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650
ataaaattcaa tacacagttc agtgcatttgc ccgttatttgc tccgaatgaa 2700
ctctaaagac aatgtacaag agactcaat ctaaaacatt tacagagtta 2750
caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800
tgactggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaaacaa 2850
aaaagaaaaag aaatttattt attaaaaattt ctattgtat ctaaaggcaga 2900
caaaaa 2906

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

Met Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
1 5 10 15

Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
20 25 30

Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140 145 150

Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
155 160 165

Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
170 175 180

Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
185 190 195

Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
200 205 210

Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
215 220 225

Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
230 235 240

Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
245 250 255

Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
260 265 270

Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
275 280 285

Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
290 295 300

Asn Pro Trp Asn Cys Asn Cys Asp Ile Leu Trp Leu Ser Trp Trp
305 310 315
Ile Lys Asp Met Ala Pro Ser Asn Thr Ala Cys Cys Ala Arg Cys
320 325 330
Asn Thr Pro Pro Asn Leu Lys Gly Arg Tyr Ile Gly Glu Leu Asp
335 340 345
Gln Asn Tyr Phe Thr Cys Tyr Ala Pro Val Ile Val Glu Pro Pro
350 355 360
Ala Asp Leu Asn Val Thr Glu Gly Met Ala Ala Glu Leu Lys Cys
365 370 375
Arg Ala Ser Thr Ser Leu Thr Ser Val Ser Trp Ile Thr Pro Asn
380 385 390
Gly Thr Val Met Thr His Gly Ala Tyr Lys Val Arg Ile Ala Val
395 400 405
Leu Ser Asp Gly Thr Leu Asn Phe Thr Asn Val Thr Val Gln Asp
410 415 420
Thr Gly Met Tyr Thr Cys Met Val Ser Asn Ser Val Gly Asn Thr
425 430 435
Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Thr Pro
440 445 450
Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser
455 460 465
Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro
470 475 480
Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro
485 490 495
Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr
500 505 510
Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr
515 520 525
Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala
530 535 540
Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His
545 550 555
Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn
560 565 570
Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu
575 580 585
Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser
590 595 600
Tyr Lys Ser Pro Phe Asn His Thr Thr Val Asn Thr Ile Asn

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
605 610 615

Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn
620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

<210> 293

<211> 4053

<212> DNA

<213> Homo Sapien

<400> 293

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aaagaaggaa ttgaccgggc agcgcgaggg aggagcgcgc acgcgaccgc 150
gagggcgggc gtgcaccctc ggcttggaaat ttgtgcggg ccccgagcgc 200
gcgcggctg ggagcttcgg gtagagacct aggccgtgg accgcgtatga 250
gcgcgcccgg cctccgtgcg cgccgcgcgg ggttggggct gctgtgtgc 300
gcgggtctgg ggccgcgtgg ccggtccgac agcggcggtc gcggggaaact 350
cgggcagccc tctggggtag ccggccgagcg cccatgcccc actacctgcc 400
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accgaatctc agctatccca cccaaAGATGT ttaaaACTGCC ccaactgcaa 900
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

actttcaatc acttatcaag gttagatgat tcaagttcc ttggcctaag 1250
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attgtgcctt ccggggcctt tccagttaa agactttgga tctgaagaac 1350
aatgaaattt cctggactat tgaagacatg aatggtgctt tctctggct 1400
tgacaaactg aggcgactga tactccaagg aaatcgatc cgttcttatta 1450
ctaaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500
gacaacgcaa tcatgtctt acaaggcaat gcattttcac aaatgaagaa 1550
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taaaatggct cccacagtgg gtggcgaaa acaactttca gagctttgta 1650
aatgccagtt gtgcccattcc tcagctgcta aaaggaagaa gcattttgc 1700
tgtagccca gatggctttg tgtgtgatga tttcccaaa cccagatca 1750
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gaggaatgaa gattgcagca ttaccaacac agatgagacc aacttgccag 2800

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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atattgacaa tagcagtgaa gctgatgtgg aagctgccac agatctgttc 3000
ctttgtccgt ttttggatc cacaggccct atgtattga agggaaatgt 3050
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caagaacagt tttaatggac cactatgagc ccagttacat aaagaaaaag 3150
gagtgctacc catgttctca tccttcagaa gaatcctgag aacggagctt 3200
cagtaatata tcgtggcctt cacatgtgag gaagctactt aacactagtt 3250
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tttaataaaaa tgtgtcaatt tgaaaaaaaaaaaaaaaaaaaaaaaaa 4050
aaa 4053

<210> 294

<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

Met Ser Ala Pro Ser Leu Arg Ala Arg Ala Ala Gly Leu Gly Leu
1 5 10 15

Leu Leu Cys Ala Val Leu Gly Arg Ala Gly Arg Ser Asp Ser Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
20 25 30

Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg
35 40 45

Pro Cys Pro Thr Thr Cys Arg Cys Leu Gly Asp Leu Leu Asp Cys
50 55 60

Ser Arg Lys Arg Leu Ala Arg Leu Pro Glu Pro Leu Pro Ser Trp
65 70 75

Val Ala Arg Leu Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
80 85 90

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
95 100 105

Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
110 115 120

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
125 130 135

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
140 145 150

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
155 160 165

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
170 175 180

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
185 190 195

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys
200 205 210

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn
215 220 225

Lys Ile Lys Asn Val Asp Gly Leu Thr Phe Gln Gly Leu Gly Ala
230 235 240

Leu Lys Ser Leu Lys Met Gln Arg Asn Gly Val Thr Lys Leu Met
245 250 255

Asp Gly Ala Phe Trp Gly Leu Ser Asn Met Glu Ile Leu Gln Leu
260 265 270

Asp His Asn Asn Leu Thr Glu Ile Thr Lys Gly Trp Leu Tyr Gly
275 280 285

Leu Leu Met Leu Gln Glu Leu His Leu Ser Gln Asn Ala Ile Asn
290 295 300

Arg Ile Ser Pro Asp Ala Trp Glu Phe Cys Gln Lys Leu Ser Glu
305 310 315

Leu Asp Leu Thr Phe Asn His Leu Ser Arg Leu Asp Asp Ser Ser
320 325 330

Phe Leu Gly Leu Ser Leu Leu Asn Thr Leu His Ile Gly Asn Asn

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
335 340 345

Arg Val Ser Tyr Ile Ala Asp Cys Ala Phe Arg Gly Leu Ser Ser
350 355 360
Leu Lys Thr Leu Asp Leu Lys Asn Asn Glu Ile Ser Trp Thr Ile
365 370 375
Glu Asp Met Asn Gly Ala Phe Ser Gly Leu Asp Lys Leu Arg Arg
380 385 390
Leu Ile Leu Gln Gly Asn Arg Ile Arg Ser Ile Thr Lys Lys Ala
395 400 405
Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn
410 415 420
Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys
425 430 435
Leu Gln Gln Leu His Leu Asn Thr Ser Ser Leu Leu Cys Asp Cys
440 445 450
Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln
455 460 465
Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly
470 475 480
Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp
485 490 495
Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala
500 505 510
Ile Lys Gly Ser Asn Leu Ser Phe Ile Cys Ser Ala Ala Ser Ser
515 520 525
Ser Asp Ser Pro Met Thr Phe Ala Trp Lys Lys Asp Asn Glu Leu
530 535 540
Leu His Asp Ala Glu Met Glu Asn Tyr Ala His Leu Arg Ala Gln
545 550 555
Gly Gly Glu Val Met Glu Tyr Thr Thr Ile Leu Arg Leu Arg Glu
560 565 570
Val Glu Phe Ala Ser Glu Gly Lys Tyr Gln Cys Val Ile Ser Asn
575 580 585
His Phe Gly Ser Ser Tyr Ser Val Lys Ala Lys Leu Thr Val Asn
590 595 600
Met Leu Pro Ser Phe Thr Lys Thr Pro Met Asp Leu Thr Ile Arg
605 610 615
Ala Gly Ala Met Ala Arg Leu Glu Cys Ala Ala Val Gly His Pro
620 625 630
Ala Pro Gln Ile Ala Trp Gln Lys Asp Gly Gly Thr Asp Phe Pro
635 640 645
Ala Ala Arg Glu Arg Arg Met His Val Met Pro Glu Asp Asp Val

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
650 655 660

Phe Phe Ile Val Asp Val Lys Ile Glu Asp Ile Gly Val Tyr Ser
665 670 675
Cys Thr Ala Gln Asn Ser Ala Gly Ser Ile Ser Ala Asn Ala Thr
680 685 690
Leu Thr Val Leu Glu Thr Pro Ser Phe Leu Arg Pro Leu Leu Asp
695 700 705
Arg Thr Val Thr Lys Gly Glu Thr Ala Val Leu Gln Cys Ile Ala
710 715 720
Gly Gly Ser Pro Pro Lys Leu Asn Trp Thr Lys Asp Asp Ser
725 730 735
Pro Leu Val Val Thr Glu Arg His Phe Phe Ala Ala Gly Asn Gln
740 745 750
Leu Leu Ile Ile Val Asp Ser Asp Val Ser Asp Ala Gly Lys Tyr
755 760 765
Thr Cys Glu Met Ser Asn Thr Leu Gly Thr Glu Arg Gly Asn Val
770 775 780
Arg Leu Ser Val Ile Pro Thr Pro Thr Cys Asp Ser Pro Gln Met
785 790 795
Thr Ala Pro Ser Leu Asp Asp Asp Gly Trp Ala Thr Val Gly Val
800 805 810
Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
815 820 825
Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
830 835 840
Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
845 850 855
Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
860 865 870
Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
875 880 885
Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
890 895 900
Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
905 910 915
Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
920 925 930
Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
935 940 945
Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
950 955 960
Glu Pro Ser Tyr Ile Lys Lys Glu Cys Tyr Pro Cys Ser His

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
965 970 975

Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
980 985 990

Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
995 1000 1005

Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
1010 1015 1020

Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
1025 1030 1035

Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
1040 1045 1050

Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
1055 1060 1065

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1070 1075 1080

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
1085 1090 1095

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
1100 1105 1110

Asn Phe Gln Ser Tyr Asp Leu Asp Thr
1115

<210> 295

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 295

ggaaccgaat ctcagct 18

<210> 296

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 296

cctaaactga actggacca 19

<210> 297

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 297

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
ggctggagac actgaacct 19

<210> 298
<211> 24
<212> DNA
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<220>
<223> Synthetic Oligonucleotide Probe

<400> 298
acagctgcac agctcagaac agtg 24

<210> 299
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 299
cattcccaagt ataaaaattt tc 22

<210> 300
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 300
gggtcttgggt gaatgagg 18

<210> 301
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 301
gtgcctctcg gttaccacca atgg 24

<210> 302
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 302
gcggccactg ttggaccgaa ctgtaaccaa gggagaaaca gccgtcctac 50

<210> 303
<211> 28
<212> DNA
<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>
<223> Synthetic Oligonucleotide Probe

<400> 303
gccttgaca accttcagtc actagtgg 28

<210> 304
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 304
ccccatgtgt ccatgactgt tccc 24

<210> 305
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 305
tactgcctca tgacaccttc actcccttgc atcatcttag agcgg 45

<210> 306
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 306
actccaagga aatcgatcc gttc 24

<210> 307
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307
tttagcagctg aggatggca caac 24

<210> 308
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 308
actccaagga aatcgatcc gttc 24

<210> 309

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 309
gccttcactg gtttggatgc attggagcat ctagacctga gtgacaacgc 50

<210> 310
<211> 3296
<212> DNA
<213> Homo Sapien

<400> 310

caaaacttgc gtcgcggaga gcgcggcagct tgacttgaat ggaaggagcc 50
cgagcccgcg gagcgcaagct gagactgggg gagcgcggttc ggccctgtggg 100
gcgcgcgtcg ggcgcggggc gcagcaggga aggggaagct gtggtctgcc 150
ctgctccacg aggcgcact ggtgtgaacc gggagagccc ctgggtggtc 200
ccgtcccccta tccctccctt atatagaaac cttccacact gggaaaggcag 250
cggcgaggca ggagggctca tggtgagcaa ggaggccggc tggatctgcag 300
gcgcacagca ttcccgagttt acagattttt acagatacca aatggaaggc 350
gaggaggcag aacagcctgc ctgggtccat cagccctggc gcccgaggcgc 400
atctgactcg gcacccctg caggcaccat ggcccagagc cgggtgctgc 450
tgctccctgct gctgctgccc ccacagctgc acctgggacc tggatctgccc 500
gtgagggccc caggatttg ccgaagtggc ggccacagcc tggatcccgaa 550
agagaacgaa tttgcggagg aggagccggt gctggactg agccctgagg 600
agcccgccc tggcccgacc gcggtcagct gccccggaga ctgtgcctgt 650
tcccaggagg gcgtcgtgga ctgtggcggt attgacactgc gtgagttccc 700
gggggacactg cctgagcaca ccaaccaccc atctctgcag aacaaccagc 750
tggaaaagat ctaccctgag gagctctccc ggctgcaccg gctggagaca 800
ctgaacactgc aaaacaaccg cctgacttcc cgaggcgtcc cagagaaggc 850
gtttgagcat ctgaccaacc tcaattaccc gtacttgcc aataacaagc 900
tgacacttggc accccgccttc ctgccaaacg ccctgatcag tggatcttt 950
gctgccaact atctcacca gatctatggg ctcaccccttgc cccagaagcc 1000
aaacttgagg tctgtgtacc tgcacaacaa caagctggca gacgcccgggc 1050
tgccggacaa catgttcaac ggctccagca acgtcgaggt cctcatcctg 1100
tccagcaact tcctgcgcca cgtgcccaag cacctgcccgc ctgcccctgta 1150

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

caagctgcac ctcaagaaca acaagctgga gaagatcccc ccgggggcct 1200
tcagcgagct gagcagcctg cgcgagctat acctgcagaa caactacctg 1250
actgacgagg gcctggacaa cgagaccttc tggaaagctct ccagcctgga 1300
gtacctggat ctgtccagca acaacctgtc tcgggtccca gctgggctgc 1350
cgcgcagcct ggtgctgctg cacttggaga agaacgcctt ccggagcgtg 1400
gacgcgaatg tgctgacccc catccgcagc ctggagtacc tgctgctgca 1450
cagcaaccag ctgccccggc agggcatcca cccactggcc ttccaggggcc 1500
tcaagcggtt gcacacggtg cacctgtaca acaacgcgtt ggagcgcgtg 1550
cccagtggcc tgcctcgccg cgtgcgcacc ctcatgatcc tgcacaacca 1600
gatcacaggc attggccgcg aagactttgc caccacctac ttccctggagg 1650
agctcaacct cagctacaac cgcatcacca gcccacaggt gcaccgcgac 1700
gccttccgca agctgcgcct gctgcgcctg ctggacctgt cggcaaccg 1750
gctgcacacg ctgccccggc ggctgcctcg aaatgtccat gtgctgaagg 1800
tcaagcgcaa tgagctggct gccttggcac gaggggcgtt ggcgggcatg 1850
gctcagctgc gtgagctgta cctcaccaggc aaccgactgc gcagccgagc 1900
cctggggccc cgtgcctggg tggacctcgc ccatctgcag ctgctggaca 1950
tcgccccggaa tcagtcaca gagatccccg aggggctccc cgagtcactt 2000
gagttacctgt acctgcagaa caacaagatt agtgcggtgt ccccaatgc 2050
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tggctgtggg ctccgtggtg gacagtgcct tccggaggct gaagcacctg 2150
caggcttgg acattgaagg caacttagag tttggtgaca tttccaagga 2200
ccgtggccgc ttggggaaagg aaaaggagga ggaggaagag gaggaggagg 2250
aggaagagga aacaagatag tgacaaggtg atgcagatgt gacctaggat 2300
gatggaccgc cggactctt tctgcagcac acgcctgtgt gctgtgagcc 2350
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tcccacatga cacgggctga cacagtctca tatccccacc cttccacg 2450
gcgtgtccca cggccagaca catgcacaca catcacaccc tcaaacaccc 2500
agctcagcca cacacaacta ccctccaaac caccacagtc tctgtcacac 2550
ccccactacc gctgccacgc cctctgaatc atgcaggaa gggctgccc 2600
ctgccccggc acacacaggc acccattccc tccccctgct gacatgtgta 2650
tgcgtatgca tacacaccac acacacacac atgcacaagt catgtgcgaa 2700
cagccctcca aagcctatgc cacagacagc tcttggccca gccagaatca 2750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gccatagcag ctcgcccgtct gccctgtcca tctgtccgtc cggtccctgg 2800
agaagacaca agggtatcca tgctctgtgg ccaggtgcct gccaccctct 2850
ggaactcaca aaagctggct tttattcctt tcccatccta tggggacagg 2900
agccttcagg actgctggcc tggcctggcc caccctgctc ctccaggtgc 2950
tggcagtc a ctctgctaa agtccctccc tgccacgccc tggcaggaca 3000
caggcacttt tccaatgggc aagcccagtg gaggcaggat gggagagccc 3050
cctgggtgct gctggggcct tggggcagga gtgaagcaga ggtgatgggg 3100
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gttcttcagg cctgtgggg aagttccggg tgccttatt ttttattctt 3200
ttcttaaggaa aaaaatgata aaaatctcaa agctgatTTT tcttgttata 3250
aaaaaactaa tataaaagca ttatccctat ccctgcaaaa aaaaaa 3296

<210> 311
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 311
gcattggccg cgagactttg cc 22

<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 312
gcggccacgg tccttggaaa tg 22

<210> 313
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 313
tggaggagct caacctcagc tacaaccgca tcaccagccc acagg 45

<210> 314
<211> 3003
<212> DNA
<213> Homo Sapien

<400> 314
gggagggggc tccgggcgcc gcgcagcaga cctgctccgg ccgcgcgcct 50

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cgccgctgtc ctccggagc ggcagcagta gcccggcgg cgagggctgg 100
gggttcctcg agactctcg aggggcgcct cccatcgcg cccaccaccc 150
caacctgttc ctcgcgcgcc actgcgctgc gccccaggac ccgctgccc 200
acatggattt ttcctggcg ctggtgctgg tattcctcgct ctacctgcag 250
gcggccgccc agttcgacgg gaggtggccc aggcaaata tagtcatcgat 300
tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350
gccagtcttg gggacagtgt cagcctgtgt gccaaccacg atgcaaacat 400
ggtaatgtta tcgggccaaa caagtgcagat tgcatacctg gttatgctgg 450
aaaaacctgt aatcaagatc taaatgatgt tggcctgaag ccccgccct 500
gtaagcacag gtgcataac acttacggca gctacaatgt ctactgtctc 550
aacggatata tgctcatgcc ggatggttcc tgctcaatgt ccctgacctg 600
ctccatggca aactgtcagt atggctgtga tgggtttaaa ggacaaatac 650
ggtgccagtg cccatccccct ggctgcacc tggctcctga tgggaggacc 700
tgttagatgt ttgatgaatg tgctacagga agagcctcct gcccattatt 750
taggcaatgt gtcaacactt ttgggagcta catctgcagat tgcataaag 800
gcttcgatct catgtatatt ggaggcaat atcaatgtca tgacatagac 850
gaatgctcac ttggtcagta tcagtcgc agctttgctc gatgttataa 900
cgtacgtggg tcctacaatgt gcaaataatgaa agaaggatac cagggtatgt 950
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cctgccaaca gagtcagaa cacccttacc acctacaacc ccagaaaggc 1250
caaccaccgg actgacaact atagcaccag ctgcccgtac acctccagga 1300
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gggacctgtg cctgtcattc aggacacaagg tgacgggct gcactctggc 1600

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acactccagg tgtttgtgag aaaacacggc gcccacggag cagccctgtg 1650
ggaaagaaaat ggtggccatg gctggaggca aacacagatc accttgcgag 1700
gggctgacat caagagcgaa tcacaaagat gattaaggg ttggaaaaaa 1750
agatctatga tggaaaatta aaggaactgg gattattgag cctggagaag 1800
agaagactga ggggcaaacc attgatggtt ttcaagtata tgaagggttg 1850
gcacagagag ggtggcgacc agctgttctc catatgcact aagaatagaa 1900
caagaggaaa ctggcttaga ctagagtata agggagcatt tcttggcagg 1950
ggccattgtt agaatacttc ataaaaaaag aagtgtgaaa atctcagtat 2000
ctctctctct ttctaaaaaa ttagataaaa atttgcgttat ttaagatgg 2050
taaagatgtt cttacccaag gaaaagtaac aaattataga atttcccaa 2100
agatgtttg atcctactag tagtatgcag tgaaaatctt tagaactaaa 2150
taatttggac aaggcttaat ttaggcattt ccctctgac ctcctaattgg 2200
agagggattg aaaggggaag agcccaccaa atgctgagct cactgaaata 2250
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cttcgtgtgt gacaagttat cttggctgct gagaaagagt gccctgcccc 2550
acaccggcag acctttcctt cacctcatca gtatgattca gtttctctta 2600
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aggtaacaata gaaggtcttc tgtcatttaa cctggtaaaag gcagggctgg 2700
agggggaaaa taaatcatta agccttgag taacggcaga atatatggct 2750
gtagatccat ttttaatggt tcatttcctt tatggtcata taactgcaca 2800
gctgaagatg aaagggaaaa ataaatgaaa atttacattt tcgatgccaa 2850
tgatacattg cactaaactg atggaagaag ttatccaaag tactgtataa 2900
catcttggttt attatttaat gtttctaaa ataaaaatg ttagtggttt 2950
tccaaatggc ctaataaaaaa caattatttg taaataaaaa cactgttagt 3000
aat 3003

<210> 315
<211> 509
<212> PRT
<213> Homo Sapien

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 315

Met Asp Phe Leu Leu Ala Leu Val Leu Val Ser Ser Leu Tyr Leu
 1 5 10 15

Gln Ala Ala Ala Glu Phe Asp Gly Arg Trp Pro Arg Gln Ile Val
 20 25 30

Ser Ser Ile Gly Leu Cys Arg Tyr Gly Arg Ile Asp Cys Cys
 35 40 45

Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50 55 60

Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65 70 75

Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80 85 90

Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95 100 105

Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110 115 120

Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
 125 130 135

Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
 140 145 150

Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155 160 165

Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170 175 180

Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185 190 195

Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200 205 210

Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215 220 225

Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230 235 240

Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245 250 255

Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260 265 270

Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
 275 280 285

Trp Ile Pro Asp Val Gly Ser Thr Trp Trp Pro Pro Lys Thr Pro
 290 295 300

Tyr Ile Pro Pro Ile Ile Thr Asn Arg Pro Thr Ser Lys Pro Thr

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
305 310 315

Thr Arg Pro Thr Pro Lys Pro Thr Pro Ile Pro Thr Pro Pro Pro
320 325 330
Pro Pro Pro Leu Pro Thr Glu Leu Arg Thr Pro Leu Pro Pro Thr
335 340 345
Thr Pro Glu Arg Pro Thr Thr Gly Leu Thr Thr Ile Ala Pro Ala
350 355 360
Ala Ser Thr Pro Pro Gly Gly Ile Thr Val Asp Asn Arg Val Gln
365 370 375
Thr Asp Pro Gln Lys Pro Arg Gly Asp Val Phe Ser Val Leu Val
380 385 390
His Ser Cys Asn Phe Asp His Gly Leu Cys Gly Trp Ile Arg Glu
395 400 405
Lys Asp Asn Asp Leu His Trp Glu Pro Ile Arg Asp Pro Ala Gly
410 415 420
Gly Gln Tyr Leu Thr Val Ser Ala Ala Lys Ala Pro Gly Gly Lys
425 430 435
Ala Ala Arg Leu Val Leu Pro Leu Gly Arg Leu Met His Ser Gly
440 445 450
Asp Leu Cys Leu Ser Phe Arg His Lys Val Thr Gly Leu His Ser
455 460 465
Gly Thr Leu Gln Val Phe Val Arg Lys His Gly Ala His Gly Ala
470 475 480
Ala Leu Trp Gly Arg Asn Gly Gly His Gly Trp Arg Gln Thr Gln
485 490 495
Ile Thr Leu Arg Gly Ala Asp Ile Lys Ser Glu Ser Gln Arg
500 505

<210> 316

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 316

gatggttcct gctcaagtgc cctg 24

<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgacttgtt aggacccacg tacg 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

ctgatggag gacctgtgta gatgttgatg aatgtgctac aggaagagcc 50

<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

<400> 319

cttcttgaa aaggattatc acctgatcag gttctcttg catttgcccc 50

tttagattgt gaaatgtggc tcaaggtctt cacaacttgc cttccctttg 100

caacaggtgc ttgctcgggg ctgaaggtga cagtgcacatc acacactgtc 150

catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200

cactccagca tcagacatcc agatcatatg gctatttgag agacccca 250

caatgccccaa atacttactg ggctctgtga ataagtctgt ggttcctgac 300

ttgaaatacc aacacaagtt caccatgatg ccacccaatg catctctgct 350

tatcaaccca ctgcagttcc ctgatgaagg caattacatc gtgaaggtca 400

acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450

gttgcgtatc ctgtcacaaa gccagtggtg cagattcatc ctccctctgg 500

ggctgtggag tatgtgggaa acatgaccct gacatgccat gtggaaagggg 550

gcactcggct agcttaccaa tggctaaaaaa atgggagacc tgtccacacc 600

agctccaccc actcctttc tccccaaaac aatacccttc atattgctcc 650

agtaaccaag gaagacattt ggaattacag ctgcctggtg aggaaccctg 700

tcagtgaaat ggaaagtgtat atcattatgc ccatcatata ttatggacct 750

tatggacttc aagtgaattt tgataaaggc ctaaaagttag gggaaagtgtt 800

tactgttgac cttggagagg ccatcctatt tgattttct gctgattctc 850

atccccccaa cacctactcc tggatttagga ggactgacaa tactacatat 900

atcattaagc atgggcctcg cttagaagtt gcatctgaga aagtagccca 950

gaagacaatg gactatgtgt gctgtgctt caacaacata accggcaggc 1000

aagatgaaac tcatttcaca gttatcatca cttccgtagg actggagaag 1050

cttgcacaga aaggaaaatc attgtcacct ttagcaagta taactggaat 1100

atcactatcc ttgatttatat ccatgtgtct tctcttcata tgaaaaaat 1150

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

atcaacccta caaagttata aaacagaaac tagaaggcag gccagaaaca 1200
gaatacagga aagctcaaac atttcaggc catgaagatg ctctggatga 1250
cttcggaata tatgaatttg ttgctttcc agatgttct ggtgttcca 1300
ggattccaag caggtctgtt ccagcctctg attgtgtatc ggggcaagat 1350
ttgcacagta cagtgtatga agttattcag cacatccctg cccagcagca 1400
agaccatcca gagtgaactt tcatgggcta aacagtacat tcgagtgaaa 1450
ttctgaagaa acatttaag gaaaaacagt gaaaaagtat attaatctgg 1500
aatcagtgaa gaaaccagga ccaacacctc ttactcatta ttcctttaca 1550
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tcataagttt tgtatgaaat atctctacaa acctaattt gttctactct 1750
acactttcac tatcatcaac actgagacta tcctgtctca cctacaaatg 1800
tggaaacttt acattgttcg attttcagc agacttgcgt ttattaaatt 1850
tttatttagt ttaagaatgc taaaattatg tttcaatttt atttccaaat 1900
ttctatctt ttatttgac aacaaagtaa taaggatggt tgtcacaaaa 1950
acaaaaactat gccttcttt tttttcaat caccagtagt attttgaga 2000
agacttgcgt acaacttaagg aaatgactat taaagtctta tttttatattt 2050
tttcaaggaa agatggattc aaataaaatta ttctgtttt gctttaaaa 2100
aaaaaaaaaa 2110

<210> 320

<211> 450

<212> PRT

<213> Homo Sapien

<400> 320

Met Trp Leu Lys Val Phe Thr Thr Phe Leu Ser Phe Ala Thr Gly
1 5 10 15

Ala Cys Ser Gly Leu Lys Val Thr Val Pro Ser His Thr Val His
20 25 30

Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe
35 40 45

His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60

Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
65 70 75

Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
85 105
90

Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu
95 100 105
Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu
110 115 120
Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr
125 130 135
Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr
140 145 150
Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg
155 160 165
Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser
170 175 180
Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala
185 190 195
Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg
200 205 210
Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile
215 220 225
Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu
230 235 240
Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu
245 250 255
Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp
260 265 270
Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro
275 280 285
Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp
290 295 300
Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu
305 310 315
Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
320 325 330
Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly
335 340 345
Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp
350 355 360
Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly
365 370 375
Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His
380 385 390
Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro
410 415 420

Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr
425 430 435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu
440 445 450

<210> 321

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 321

gatcctgtca caaagccagt ggtgc 25

<210> 322

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

ctccctctgg gctgtggagt atgtgggaa catgaccctg acatg 45

<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

gcaagcggcg aaatggcgcc ctccggaggt cttgcagttc ccctggcagt 50

cctggtgctg ttgctttggg gtgctccctg gacgcacggg cggcggagca 100

acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aattttatgc cccgtggtgc cctgcttgct aaaatcttca 200

accggaatgg gaaagtttg ctgaatgggg agaagatctt gaggttaata 250

ttgcgaaagt agatgtcaca gagcagccag gactgagtgg acggtttatac 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ataactgctc ttccctactat ttatcattgt aaagatggtg aatttaggcg 350
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aagagtggaa gagtattgag cccgtttcat catggttgg tccaggttct 450
gttctgatga gtagtatgtc agcaactctt cagctatcta tgtggatcag 500
gacgtgccat aactacttta ttgaagacct tggattgcca gtgtggggat 550
catatactgt ttttgcttta gcaactctgt tttccggact gttatttagga 600
ctctgtatga tatttggc agattgcctt tgccttcaa aaaggcgcag 650
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gaatgccata agacaacgct ctctgggtcc atcattggcc acagataaat 850
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aagattgatc atttgtttg gttgaagtg aactgtgact ttttgaata 950
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tgttcttcc tgactggtaa tattgtgtgg gatttcacag gtaaaagtca 2050
taggatgga acattttagt gtattttac tccttaaaga gctagaatac 2100
atagtttca ccttaaaaga agggggaaaa tcataaatac aatgaatcaa 2150
ctgaccatta cgttagtagac aatttctgta atgtccctt ctttcttaggc 2200
tctgttgctg tgtgaatcca ttagatttac agtatcgtaa tatacaagtt 2250
ttcttaaag ccctctcctt tagaatttaa aatattgtac cattaaagag 2300
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aaaccttctt aaccacttca ttaaagctga aaaaaaaaaa aaaaaaaa 2397

<210> 325
<211> 280
<212> PRT

<213> Homo Sapien

<400> 325
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Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly
35 40 45
Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln
50 55 60
Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75
Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90
Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
95 100 105
Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys
110 115 120
Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile
125 130 135
Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser
140 145 150
Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys
155 160 165
His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser
170 175 180

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195
Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210
Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
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<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
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<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtctagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttccctgt gcagtcctgg tgctgttgc ttggg 45

<210> 331
<211> 2168
<212> DNA
<213> Homo Sapien

<400> 331
gcgaggtgtcc agctgcggag acccggtata attcgtaac taattcaaca 50
aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taacccagtg 100
ggacaggcgg atttggaaagag cggaaaggc tcggccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
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caatgctgag tgtggatgac tgctttggga tggggccgtc ggctacaat 700
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gaatctgcgg tactttgagc agttatttggaa ggaagagaga gaaaaaacgt 950
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aggcctgtgg actacacctgcc tgagagggat gtttacgaga gcctctgtcg 1050

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gtctgatgag gaaatcgaga gcatcaagga gatcgcaaaa cctaaacttg 1250
cacgagccac cggtcgat cccaaagacag gagtcctcac tgtcgccagc 1300
taccgggtt cccaaagctc ctggctagag gaagatgatg accctgttgt 1350
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ctgcagaatt gttacaggtt gcaaattatg gagtgggagg acagtatgaa 1450
ccgcacttcg acttctctag gcgacctttt gacagcggcc tccaaacaga 1500
ggggaaatagg ttagcgacgt ttcttaacta catgagtatgat gttagaagctg 1550
gtggtgccac cgtctccct gatctgggg ctgcaatttg gcctaagaag 1600
ggtacagctg tggtctggta caacctcttg cggagcgggg aaggtgacta 1650
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tcaacagaag ttgactgaca tcctttctg tccttccct tcctggctc 1800
tcagccatg tcaacgtgac agacacctt gtatgtcct ttgtatgttc 1850
ctatcaggct gattttgga gaaatgaatg ttgtctggta gcagagggag 1900
accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950
gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000
gttagctgctc tagcgcttag caaggtgcct ttgtacctca ggtgttttag 2050
gtgtgagatg tttcagtgaa ccaaagttct gataccttgtt ttacatgttt 2100
gttttatgg catttctatc tattgtggct ttaccaaaaa ataaaatgtc 2150
cctaccagaa aaaaaaaaa 2168

<210> 332
<211> 533
<212> PRT
<213> Homo Sapien

<400> 332

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Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met

	20				25					30				
--	----	--	--	--	----	--	--	--	--	----	--	--	--	--

Thr Asp Leu Ile Tyr Ala Glu Glu Leu Val Gln Ser Leu Lys

		35				40				45				
--	--	----	--	--	--	----	--	--	--	----	--	--	--	--

Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser

		50				55				60				
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Trp Ala Asn Lys Met Glu Ala Leu Thr Ser Lys Ser Ala Ala Asp
65 70 75
Ala Glu Gly Tyr Leu Ala His Pro Val Asn Ala Tyr Lys Leu Val
80 85 90
Lys Arg Leu Asn Thr Asp Trp Pro Ala Leu Glu Asp Leu Val Leu
95 100 105
Gln Asp Ser Ala Ala Gly Phe Ile Ala Asn Leu Ser Val Gln Arg
110 115 120
Gln Phe Phe Pro Thr Asp Glu Asp Glu Ile Gly Ala Ala Lys Ala
125 130 135
Leu Met Arg Leu Gln Asp Thr Tyr Arg Leu Asp Pro Gly Thr Ile
140 145 150
Ser Arg Gly Glu Leu Pro Gly Thr Lys Tyr Gln Ala Met Leu Ser
155 160 165
Val Asp Asp Cys Phe Gly Met Gly Arg Ser Ala Tyr Asn Glu Gly
170 175 180
Asp Tyr Tyr His Thr Val Leu Trp Met Glu Gln Val Leu Lys Gln
185 190 195
Leu Asp Ala Gly Glu Glu Ala Thr Thr Thr Lys Ser Gln Val Leu
200 205 210
Asp Tyr Leu Ser Tyr Ala Val Phe Gln Leu Gly Asp Leu His Arg
215 220 225
Ala Leu Glu Leu Thr Arg Arg Leu Leu Ser Leu Asp Pro Ser His
230 235 240
Glu Arg Ala Gly Gly Asn Leu Arg Tyr Phe Glu Gln Leu Leu Glu
245 250 255
Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu
260 265 270
Ala Thr Pro Glu Gly Ile Tyr Glu Arg Pro Val Asp Tyr Leu Pro
275 280 285
Glu Arg Asp Val Tyr Glu Ser Leu Cys Arg Gly Glu Gly Val Lys
290 295 300
Leu Thr Pro Arg Arg Gln Lys Arg Leu Phe Cys Arg Tyr His His
305 310 315
Gly Asn Arg Ala Pro Gln Leu Leu Ile Ala Pro Phe Lys Glu Glu
320 325 330
Asp Glu Trp Asp Ser Pro His Ile Val Arg Tyr Tyr Asp Val Met
335 340 345
Ser Asp Glu Glu Ile Glu Arg Ile Lys Glu Ile Ala Lys Pro Lys
350 355 360
Leu Ala Arg Ala Thr Val Arg Asp Pro Lys Thr Gly Val Leu Thr
365 370 375

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Ala Ser Tyr Arg Val Ser Lys Ser Ser Trp Leu Glu Glu Asp
380 385 390
Asp Asp Pro Val Val Ala Arg Val Asn Arg Arg Met Gln His Ile
395 400 405
Thr Gly Leu Thr Val Lys Thr Ala Glu Leu Leu Gln Val Ala Asn
410 415 420
Tyr Gly Val Gly Gly Gln Tyr Glu Pro His Phe Asp Phe Ser Arg
425 430 435
Arg Pro Phe Asp Ser Gly Leu Lys Thr Glu Gly Asn Arg Leu Ala
440 445 450
Thr Phe Leu Asn Tyr Met Ser Asp Val Glu Ala Gly Gly Ala Thr
455 460 465
Val Phe Pro Asp Leu Gly Ala Ala Ile Trp Pro Lys Lys Gly Thr
470 475 480
Ala Val Phe Trp Tyr Asn Leu Leu Arg Ser Gly Glu Gly Asp Tyr
485 490 495
Arg Thr Arg His Ala Ala Cys Pro Val Leu Val Gly Cys Lys Trp
500 505 510
Val Ser Asn Lys Trp Phe His Glu Arg Gly Gln Glu Phe Leu Arg
515 520 525
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530

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

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<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 335
ggtctcaaga actcctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
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<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cttctacaac gctgactacc tggcgccccg agcccgctg gcaggtgaac 2400
tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450
gtttcctcc gtttctcagg gctccacctc tttcggccg tagagccagg 2500
gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcagtgaag 2550
aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600
gcccagctgg ctatggctct cttttagcag gagcaggcca atagcactta 2650
gcccgcctgg gggccctaac ctcattacct ttcctttgtc tgcctcagcc 2700
ccaggaaggg caaggcaaga tggtagcag atagagaatt gttgctgtat 2750
tttttaaata tgaaaatgtt attaaacatg tcttctgcc 2789

<210> 339

<211> 772

<212> PRT

<213> Homo Sapien

<400> 339

Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
1 5 10 15

Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
20 25 30

Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
35 40 45

Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
50 55 60

Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
65 70 75

Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Val Leu Arg Thr Arg
80 85 90

Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala
95 100 105

Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val
110 115 120

Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr
125 130 135

Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser
140 145 150

His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg
155 160 165

His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile
170 175 180

Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu
185 190 195

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly His Leu Ser Ile Asn Gln Asp Leu Tyr Leu Gly Arg Ala 210
 200 205 210
 Glu Glu Phe Ile Gly Ala Gly Glu Gln Ala Arg Tyr Cys His Gly 225
 215 220 225
 Gly Phe Gly Tyr Leu Leu Ser Arg Ser Leu Leu Leu Arg Leu Arg 240
 230 235 240
 Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro 255
 245 250 255
 Asp Glu Trp Leu Gly Arg Cys Leu Ile Asp Ser Leu Gly Val Gly 270
 260 265 270
 Cys Val Ser Gln His Gln Gly Gln Gln Tyr Arg Ser Phe Glu Leu 285
 275 280 285
 Ala Lys Asn Arg Asp Pro Glu Lys Glu Gly Ser Ser Ala Phe Leu 300
 290 295 300
 Ser Ala Phe Ala Val His Pro Val Ser Glu Gly Thr Leu Met Tyr 315
 305 310 315
 Arg Leu His Lys Arg Phe Ser Ala Leu Glu Leu Glu Arg Ala Tyr 330
 320 325 330
 Ser Glu Ile Glu Gln Leu Gln Ala Gln Ile Arg Asn Leu Thr Val 345
 335 340 345
 Leu Thr Pro Glu Gly Glu Ala Gly Leu Ser Trp Pro Val Gly Leu 360
 350 355 360
 Pro Ala Pro Phe Thr Pro His Ser Arg Phe Glu Val Leu Gly Trp 375
 365 370 375
 Asp Tyr Phe Thr Glu Gln His Thr Phe Ser Cys Ala Asp Gly Ala 390
 380 385 390
 Pro Lys Cys Pro Leu Gln Gly Ala Ser Arg Ala Asp Val Gly Asp 405
 395 400 405
 Ala Leu Glu Thr Ala Leu Glu Gln Leu Asn Arg Arg Tyr Gln Pro 420
 410 415 420
 Arg Leu Arg Phe Gln Lys Gln Arg Leu Leu Asn Gly Tyr Arg Arg 435
 425 430 435
 Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr Leu Asp Leu Leu Leu 450
 440 445 450
 Glu Cys Val Thr Gln Arg Gly His Arg Arg Ala Leu Ala Arg Arg 465
 455 460 465
 Val Ser Leu Leu Arg Pro Leu Ser Arg Val Glu Ile Leu Pro Met 480
 470 475 480
 Pro Tyr Val Thr Glu Ala Thr Arg Val Gln Leu Val Leu Pro Leu 495
 485 490 495
 Leu Val Ala Glu Ala Ala Ala Ala Pro Ala Phe Leu Glu Ala Phe 510
 500 505 510

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
515 520 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
530 535 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
545 550 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
560 565 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
575 580 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
590 595 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
605 610 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
635 640 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
650 655 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
665 670 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
680 685 690

Ala Gly Gln Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
695 700 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
710 715 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
725 730 735

Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
755 760 765

Gln Glu Gln Ala Asn Ser Thr
770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cgagatggtg cgccaacgtg agagggaaacc cgtgcgcggc tgcgcgttcc 50

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgtccccaaag ccgttctaga cgcggggaaaa atgcttctg aaagcagctc 100
cttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgcttaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatcttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtcttggg ctgcagtaaa ggagacttgg 350
accaaacact gtgacaaagc agagttctc agttctgaaa atgttaaagt 400
gtttgagtca attaatatgg acacaaatga catgtggta atgatgagaa 450
aagcttacaa atacgcctt gataagtata gagaccaata caactggttc 500
ttccttgcac gccccactac gtttgcatac attgaaaacc taaagtattt 550
tttgttaaaa aaggatccat cacagcctt ctatctaggc cacactataa 600
aatctggaga ccttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagtg 700
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
cagttgcct gaaatatgct ggagtatttgc cagaaaatgc agaagatgct 800
gatggaaaag atgtattna taccaaattct gttggcctt ctattaaaga 850
ggcaatgact tattttttttt accaggtgtt agaaggctgt tgttcagata 900
tggctgttac tttaatggc ctgactccaa atcagatgca tgtgtatgt 950
tatgggtat accgccttag ggcatttggg catatttca atgatgcatt 1000
ggtttctta cctccaaatg gttctgacaa tgactgagaa gtggtagaaa 1050
agcgtgaata tgatcttgc ataggacgtg tggtgtcatt attttagta 1100
gttaactacat atccaaataca gctgtatgtt tcttttctt ttctaaatttgc 1150
gtggcactgg tataaccaca cattaaatgc agtagtacat tttaatgg 1200
gggtgggtttt ttctttaaa acacatgaac attgtaaatg tggtggaaag 1250
aagtgtttta agaataataa ttgtcaaat aaactattaa taaatattat 1300
atgtgataaa ttctaaatggc tgaacatttttgc aatctgtgg ggcacatatttgc 1350
tttgctgatt ggtttttttt tttaacagg tcttttagcgt tctaaatgg 1400
gcaaatgata tctctagtttgc tgaatttgcgtt attaaatggc aacttttagc 1450
tgtgtgttcc cttaacttctt aatactgatttgc tatgttctaa gcctccccaa 1500
gttccaaatggc atttgccttc tcaaaatggc caactaagca actaaagaaa 1550
attaaatggc aagttggaaaa at 1572

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 318
<212> PRT
<213> Homo Sapien

<400> 341

Met Leu Ser Glu Ser Ser Ser Phe Leu Lys Gly Val Met Leu Gly
1 5 10 15

Ser Ile Phe Cys Ala Leu Ile Thr Met Leu Gly His Ile Arg Ile
20 25 30

Gly His Gly Asn Arg Met His His His Glu His His His His Leu Gln
35 40 45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
50 55 60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val
65 70 75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp
80 85 90

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val
95 100 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu
110 115 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp
125 130 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile
140 145 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
155 160 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr
170 175 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys
185 190 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
200 205 210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
215 220 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
230 235 240

Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
245 250 255

Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
260 265 270

Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
275 280 285

Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
290 295 300
295 300 305 310 315

His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser
305 310 315

Asp Asn Asp

<210> 342

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 342

tccccaagcc gttctagacg cg 23

<210> 343

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 344

gcccaaatgc cctaaggcgg tatacccc 28

<210> 345

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 345

gggtgtgatg cttggaagca ttttctgtgc tttgatcact atgctaggac 50

<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

gggatgcagg tggtgtctca tgggg 25

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 347

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 347

ccctcatgt a ccggctcc 18

<210> 348

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 348

ggattctaat acgactcact atagggctca gaaaagcgca acagagaa 48

<210> 349

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 349

ctatgaaatt aaccctcact aaagggatgt cttccatgcc aacctc 47

<210> 350

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 350

ggattctaat acgactcact atagggcggc gatgtccact ggggctac 48

<210> 351

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 351

ctatgaaatt aaccctcact aaagggacga ggaagatggg cggatggt 48

<210> 352

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 352
ggattctaat acgactcact atagggcacc cacgcgtccg gctgctt 47

<210> 353
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 353
ctatgaaatt aaccctcact aaagggacgg gggacaccac ggaccaga 48

<210> 354
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 354
ggattctaat acgactcact atagggcttg ctgcggttt tggccttg 48

<210> 355
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 355
ctatgaaatt aaccctcact aaagggagct gccgatccca ctggatt 48

<210> 356
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 356
ggattctaat acgactcact atagggcgga tcctggccgg cctctg 46

<210> 357
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 357
ctatgaaatt aaccctcact aaagggagcc cgggcatggt ctcagtta 48

<210> 358
<211> 47
<212> DNA
<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>
<223> Synthetic Oligonucleotide Probe

<400> 358
ggattctaat acgactcaact atagggcggg aagatggcga ggaggag 47

<210> 359
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 359
ctatgaaatt aaccctcaact aaagggacca aggccacaaa cgaaatc 48

<210> 360
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 360
ggattctaat acgactcaact atagggctgt gctttcattc tgccagta 48

<210> 361
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 361
ctatgaaatt aaccctcaact aaagggaggg tacaattaag gggtggat 48

<210> 362
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 362
ggattctaat acgactcaact atagggcccg cctcgctcct gctcctg 47

<210> 363
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 363
ctatgaaatt aaccctcaact aaagggagga ttgccgcgac cctcacag 48

<210> 364
<211> 47

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 364

ggattctaat acgactcact atagggcccc tcctgccttc cctgtcc 47

<210> 365

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 365

ctatgaaatt aaccctcact aaagggagtg gtggccgcga ttatctgc 48

<210> 366

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 366

ggattctaat acgactcact atagggcgca gcgatggcag cgatgagg 48

<210> 367

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 367

ctatgaaatt aaccctcact aaagggacag acggggcaga gggagtg 47

<210> 368

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 368

ggattctaat acgactcact atagggccag gaggcgtgag gagaac 47

<210> 369

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 369

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

ctatgaaatt aaccctcaact aaaggaaag acatgtcatc gggagtgg 48

<210> 370
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 370
ggattctaat acgactcaact atagggccgg gtggaggtgg aacagaaa 48

<210> 371
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 371
ctatgaaatt aaccctcaact aaaggacac agacagagcc ccatacgc 48

<210> 372
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 372
ggattctaat acgactcaact atagggccag ggaaatccgg atgtctc 47

<210> 373
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 373
ctatgaaatt aaccctcaact aaaggagta agggatgcc accgagta 48

<210> 374
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 374
ggattctaat acgactcaact atagggccag ctacccgcag gaggagg 47

<210> 375
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Synthetic Oligonucleotide Probe

<400> 375
ctatgaaatt aaccctcact aaagggatcc caggtgatga ggtccaga 48

<210> 376

<211> 997

<212> DNA

<213> Homo Sapien

<400> 376
cccacgcgtc cgatcttacc aacaaaacac tcctgaggag aaagaaaagag 50
agggagggag agaaaaagag agagagagaa acaaaaaacc aaagagagag 100
aaaaaaatgaa ttcatctaaa tcatctgaaa cacaatgcac agagagagga 150
tgcttctctt cccaaatgtt cttatggact gttgctggga tccccatcct 200
atttctcagt gcctgtttca tcaccagatg ttttgtgaca tttcgcatct 250
ttcaaacctg tgatgagaaa aagtttcagc tacctgagaa tttcacagag 300
ctctcctgct acaattatgg atcaggttca gtcaagaatt gttgtccatt 350
gaactggaa tattttcaat ccagctgcta cttctttctt actgacacca 400
tttcctggc gttaagtttta aagaactgct cagccatggg ggctcacctg 450
gtggatca actcacagga ggagcaggaa ttcccttcata acaagaaaacc 500
taaaatgaga gagttttta ttggactgtc agaccaggaa gtcgagggtc 550
agtggcaatg ggtggacggc acaccttga caaaatctt gaggctctgg 600
gatgttagggg agcccaacaa catagctacc ctggaggact gtgccaccat 650
gagagactct tcaaacccaa ggcaaaatttgaatgtatgtt acctgtttcc 700
tcaattatgtt tcggattttgt gaaatggtag gaataaatcc tttgaacaaa 750
ggaaaatctc tttaagaaca gaaggcacaa ctcaaatgtg taaagaagga 800
agagcaagaa catggccaca cccaccggccc cacacgagaa atttgcgc 850
tgaacttcaa aggacttcat aagtattttgt tactctgata caaataaaaa 900
taagtagttt taaatgttaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 997

<210> 377

<211> 219

<212> PRT

<213> Homo Sapien

<400> 377
Met Asn Ser Ser Lys Ser Ser Glu Thr Gln Cys Thr Glu Arg Gly
1 5 10 15
Cys Phe Ser Ser Gln Met Phe Leu Trp Thr Val Ala Gly Ile Pro
20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile	Leu	Phe	Leu	Ser	Ala	Cys	Phe	Ile	Thr	Arg	Cys	Val	Val	Thr
35								40						45
Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro														
50								55						60
Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser														
65								70						75
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser														
80								85						90
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu														
95								100						105
Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser														
110								115						120
Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg														
125								130						135
Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp														
140								145						150
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp														
155								160						165
Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala														
170								175						180
Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val														
185								190						195
Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile														
200								205						210
Asn Pro Leu Asn Lys Gly Lys Ser Leu														
215														

<210> 378

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 378

ttcagttct gggatgtagg g 21

<210> 379

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 379

tattcctacc atttcacaaa tccg 24

<210> 380

<211> 49

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 380

ggaggactgt gccaccatga gagactcttc aaacccaagg caaaaattgg 49

<210> 381

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

gcagatttg aggacagcca cctcca 26

<210> 382

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

ggccttgcag acaaccgt 18

<210> 383

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

cagactgagg gagatccgag a 21

<210> 384

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 384

cagctgccct tcccccaacca 20

<210> 385

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 385

catcaagcgc ctctacca 18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 386
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 386
cacaactcg aactgcttct g 21

<210> 387
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 387
gggccatcac agtccct 18

<210> 388
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 388
gggatgtggtaa acacacagaa ca 22

<210> 389
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 389
tgccagctgc atgctgccag tt 22

<210> 390
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 390
cagaaggatg tcccggtggaa 20

<210> 391
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<213> Artificial Sequence

<220>

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Synthetic oligonucleotide probe

<400> 391
gccgctgtcc actgcag 17

<210> 392
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 392
gacggcatcc tcagggccac a 21

<210> 393
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 393
atgtcctcca tgcccacgct 20

<210> 394
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 394
gagtgcgaca tcgagagctt 20

<210> 395
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
ccgcagcctc agtgatga 18

<210> 396
<211> 21
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 396
gaagagcaca gctgcagatc c 21

<210> 397
<211> 22
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

gaggtgtcct ggctttggta gt 22

<210> 398

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

cctctggcgc ccccaactcaa 20

<210> 399

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 399

ccagagagc tggcgatg 18

<210> 400

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 400

gcaaattcag ggctcactag aga 23

<210> 401

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

cacagagcat ttgtccatca gcagttcag 29

<210> 402

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 402

ggcagagact tccagtcact ga 22

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 403

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

gccaaagggtg gtgttagata gg 22

<210> 404

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 404

caggccccct tcatctgtac ccca 24

<210> 405

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 405

gggacgtgct tctacaagaa cag 23

<210> 406

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

caggcttaca atgttatgtat cagaca 26

<210> 407

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

tattcagagt tttccattgg cagtgccagt t 31

<210> 408

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 408
tctacatcag cctctctgcg c 21

<210> 409
<211> 23
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<220>
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<400> 409
cgatcttctc cacccaggag cg 23

<210> 410
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 410
gccaggcctc acattcgt 18

<210> 411
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 411
ctccctgaat ggcagcctga gca 23

<210> 412
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 412
agggtttat taagggccta cgct 24

<210> 413
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 413
cagagcagag ggtgccttg 19

<210> 414
<211> 21
<212> DNA
<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>
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<400> 414
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<210> 415
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 415
ccctgttcc ctatgcata ct 22

<210> 416
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 416
tcaacccttg accctttcct a 21

<210> 417
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 417
ggcaggggac aagccatctc tcct 24

<210> 418
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 418
gggactgaac tgccagcttc 20

<210> 419
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 419
gggccttaac ctcattacct tt 22

<210> 420

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 420

tgtctgcctc agccccagga agg 23

<210> 421

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 421

tctgtccacc atttgcctt g 21

<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

<400> 422

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atggcgctga ggcggccacc gcgactccgg ctctgcgctc ggctgcctga 100

cttcttcctg ctgctgcctt tcaggggctg cctgataggg gctgtaaatc 150

tcaaatccag caatcgaacc ccagtggta aggaatttga aagtgtggaa 200

ctgtcttgca tcattacgga ttgcagaca agtgacccca ggatcgagtg 250

gaagaaaatt caagatgaac aaaccacata tgtgttttt gacaacaaaa 300

ttcagggaga cttggcggtt cgtgcagaaa tactggggaa gacatccctg 350

aagatctgga atgtgacacg gagagactca gcccttatac gctgtgaggt 400

cgttgctcga aatgaccgca agggaaattga ttagattgtg atcgagttaa 450

ctgtgcaagt gaagccagtg accccctgtct gtagagtgcc gaaggctgta 500

ccagtaggca agatggcaac actgcactgc caggagagtg agggccaccc 550

ccggcctcac tacagctggt atcgcaatga tgtaccactg cccacggatt 600

ccagagccaa tcccagattt cgcaattctt ctttccactt aaactctgaa 650

acaggcactt tgggtttcac tgctgttac aaggacgact ctgggcagta 700

ctactgcatt gtttccaatg acgcaggctc agccaggtgt gaggagcagg 750

agatggaagt ctatgacctg aacattggcg gaattattgg gggggttctg 800

gttgccttg ctgtactggc cctgatcacg ttgggcatct gctgtgcata 850

cagacgtggc tacttcatca acaataaaca ggatggagaa agttacaaga 900

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

acccaggaa accagatgga gttaactaca tccgcactga cgaggaggc 950
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ttttcgaaaa ggccaaagtt gaccactact cttcttactc taacaagcca 1150
catgaataga agaattttcc tcaagatgga cccggtaaat ataaccacaa 1200
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tgcgaaatca agtctgtcaa gtacaataac atttttaaaaaaa gaaaatggat 2550
cccactgttc ctcttgcca cagagaaagc acccagacgc cacaggctct 2600
gtcgcatttc aaaacaaacc atgatggagt ggcggccagt ccagccttt 2650
aaagaacgac aggtggagca gccaggtgaa aggctggcg gggagggaaag 2700
tgaaacgcct gaatcaaaag cagtttcta attttgactt taaattttc 2750
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gccttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500
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ccca 3554

<210> 423
<211> 310
<212> PRT
<213> Homo Sapien

<400> 423
Met Ala Leu Arg Arg Pro Pro Arg Leu Arg Leu Cys Ala Arg Leu
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Pro Asp Phe Phe Leu Leu Leu Phe Arg Gly Cys Leu Ile Gly
20 25 30
Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
35 40 45
Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Asp Pro Arg Ile Glu Trp Lys Lys Ile Gln Asp Glu Gln Thr
65 70 75

Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
185 190 195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
275 280 285

Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
305 310